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OM nucleic - nucleic search, using sw model

Run on: November 22, 2002, 22:13:53 ; Search time 3186 Seconds

(without alignments)
7796.854 Million cell updates/sec

Title: US-09-928-412-1

Perfect score: 988
Sequence: 1 gaattcgagccgtcccaaa.....cttgagcgccgcaatc 988

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance a
score greater than or equal to the score of the result being printed,
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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	988	100.0	988	34	US-09-928-412-1
2	577.6	58.5	783	1	PCT-US02-27884-3525
3	516.2	52.2	622	1	PCT-US02-27884-3352
4	490.2	49.6	623	1	PCT-US02-27884-3530
5	481.2	49.0	724	28	US-09-705-926-4708
6	385.8	39.0	632	1	PCT-US02-27884-3350
7	371.6	37.6	618	28	US-09-705-926-3115
8	343.4	34.8	994	41	US-10-155-881-36087
9	343.4	34.8	994	75	US-10-155-881-15914
10	342.8	34.7	1489	41	US-10-155-881-15914
11	339.6	34.4	973	41	US-10-155-881-36088
12	339.6	34.4	973	75	US-10-155-881-36088
13	338.6	34.3	1006	25	US-09-654-617-2276
14	338.6	34.3	1006	27	US-09-654-617-2276
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22 335.4 33.9 1168 31 US-09-816-660-12341 Sequence 12341, A
23 335 33.9 1063 41 US-10-155-881-36091 Sequence 36091, A
24 334.2 33.8 956 19 US-09-513-996A-62273 Sequence 62273, A
25 334.2 33.8 1042 25 US-09-654-617-124315 Sequence 124315, A
26 334.2 33.8 1042 27 US-09-684-016-124315 Sequence 124315, A
27 334.2 33.8 1042 29 US-09-733-089-2630 Sequence 2630, Ap
28 334.2 33.8 1042 31 US-09-816-660-2630 Sequence 2630, Ap
29 333 33.7 578 1 PCT-US02-27884-1066 Sequence 1066, Ap
30 332 33.6 570 22 US-09-565-309A-66976 Sequence 66976, A
31 332 33.6 969 19 US-09-513-996A-2994 Sequence 2994, Ap
32 332 33.6 969 22 US-09-565-309A-52278 Sequence 52278, A
33 332 33.6 969 22 US-09-565-309A-61940 Sequence 61940, A
34 332 33.6 969 22 US-09-595-329A-1450 Sequence 1450, A
35 331 33.5 886 19 US-09-513-996A-9337 Sequence 9337, Ap
36 330.8 33.5 711 33 US-09-874-708A-64616 Sequence 64616, A
37 330.8 33.5 711 65 US-60-211-750-63529 Sequence 63529, A
38 330.4 33.4 747 33 US-09-874-708A-69304 Sequence 69304, A
39 330.4 33.4 747 65 US-60-211-750-68213 Sequence 68213, A
40 329 33.3 1191 41 US-10-155-881-15913 Sequence 15913, A
41 324.4 32.8 701 23 US-09-605-702-10495 Sequence 10495, A
42 324.4 32.8 701 23 US-09-611-520-9806 Sequence 9806, Ap
43 324.4 32.8 701 39 US-10-075-564-9806 Sequence 9806, Ap
44 324.4 32.8 701 58 US-60-146-224-6858 Sequence 6858, Ap
45 324 32.8 521 1 PCT-US02-27884-3353 Sequence 3353, Ap

ALIGNMENTS

RESULT 1
US-09-928-412-1

Sequence 1, Application US/09928412
GENERAL INFORMATION:
APPLICANT: KANAOKA, Akiyoshi
APPLICANT: EBINUMA, Hiroyasu
TITLE OF INVENTION: TRANSCRIPTION FACTOR CONTROLLING PHENYLPROPANOID
TITLE OF INVENTION: BIOSYNTHESIS PATHWAY
FILE REFERENCE: 4859-0027-0
CURRENT APPLICATION NUMBER: US/09/928,412
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/282,146
PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 10-125171
PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 988
TYPE: DNA
ORGANISM: Nicotiana tabacum
FEATURE:
NAME/KEY: CDS
LOCATION: (100)..(702)
NAME/KEY: misc_feature
LOCATION: (127)..(282)
OTHER INFORMATION: LIM domain
NAME/KEY: misc_feature
LOCATION: (427)..(582)
OTHER INFORMATION: LIM domain
US-09-928-412-1

Query Match 100.0%; Score 988; DB 34; Length 988;
Best Local Similarity 100.0%; Pred. No. 1.2e-234;
Matches 988; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGCGCCGTTCCAAACCAAGTGTACACAAAGAAAGGAAAGCCACCAAG 60
DB 1 GAATTCGGCGCCGTTCCAAACCAAGTGTACACAAAGAAAGGAAAGCCACCAAG 60
QY 61 ACCATTTTCTTTCTGTAAACCTGCTATATAGCATGGCTTTTGAGAGAACACA 120
DB 61 ACCATTTTCTTTCTGTAAACCTGCTATATAGCATGGCTTTTGAGAGAACACA 120

QY 121 CAGAAATGCATGCATGTGACAGACGTCTATCTGTGTGACAAATTAAGTCAGATTAAC 180
DB 121 CAGAAATGCATGCATGTGACAGACGTCTATCTGTGTGACAAATTAAGTCAGATTAAC 180
QY 181 AGAATCTATCAACAAAGCTGTGTGACATGCATGACGACGACGACGACGACGACGAC 240
DB 181 AGAATCTATCAACAAAGCTGTGTGACATGCATGACGACGACGACGACGACGACGAC 240
QY 241 AACTACATTCCTTTGAGAGGAGGATCTATATCTAGACACACTTTGATTCAGCTTTGAAA 300
DB 241 AACTACATTCCTTTGAGAGGAGGATCTATATCTAGACACACTTTGATTCAGCTTTGAAA 300
QY 301 CAATCGGCACTTTGGATTAAGCTTTGAAAGTACACCAAAAAATGTGAAGCCACAGAAA 360
DB 301 CAATCGGCACTTTGGATTAAGCTTTGAAAGTACACCAAAAAATGTGAAGCCACAGAAA 360
QY 361 CCCATTGACAGTGAAGAAACACAGGTAGCCAAATGACAAAGCATGTTGGTGAACAGAA 420
DB 361 CCCATTGACAGTGAAGAAACACAGGTAGCCAAATGACAAAGCATGTTGGTGAACAGAA 420
QY 421 GAGAAATGTTTGGCTGCAAGAAACTGTCTACCCACAGAAAGTATCAGCCATGGC 480
DB 421 GAGAAATGTTTGGCTGCAAGAAACTGTCTACCCACAGAAAGTATCAGCCATGGC 480
QY 481 AGCCCATACCAATTAAGCTGCTTCAATTCAGACGACGAGGCTGTATTAAGCCCTTCC 540
DB 481 AGCCCATACCAATTAAGCTGCTTCAATTCAGACGACGAGGCTGTATTAAGCCCTTCC 540
QY 541 AACTATACCGCACATGAGGGGCGCTTATTTGTAACATACCATTAACATTAAC 600
DB 541 AACTATACCGCACATGAGGGGCGCTTATTTGTAACATACCATTAACATTAAC 600
QY 601 GAGAGGGCAACTTAAGCAAGCTTGAGGGTGACCATGAATTAATTCACAGACAAACA 660
DB 601 GAGAGGGCAACTTAAGCAAGCTTGAGGGTGACCATGAATTAATTCACAGACAAACA 660
QY 661 GGAATCTGACAGATATACACAGCCGACCAAGTATGATTCCTTAACCGCGA 720
DB 661 GGAATCTGACAGATATACACAGCCGACCAAGTATGATTCCTTAACCGCGA 720
QY 721 TCATGATTTAGTATGCTGCTGTAGTTGTAAGATGCAAGGCGTTCAGAGCTTCATGA 780
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QY 781 ATGCACCTTGGCTCCCGACGATGTTTACTTAATCTAGCTCAATTAATTTGATGT 840
DB 781 ATGCACCTTGGCTCCCGACGATGTTTACTTAATCTAGCTCAATTAATTTGATGT 840
QY 841 TGAACATATATATGTCTAGCTTTTGTGTGATTTTGAACCTTTGCTTGTGCTTC 900
DB 841 TGAACATATATATGTCTAGCTTTTGTGTGATTTTGAACCTTTGCTTGTGCTTC 900
QY 901 ACTTGATTTATGGAATGTAATGATGATGATTAATCAATGTTTGTGCTCCAGTGC 960
DB 901 ACTTGATTTATGGAATGTAATGATGATTAATCAATGTTTGTGCTCCAGTGC 960
QY 961 ATGCAAAATCTTTGAGCGCGCGCAATTC 988
DB 961 ATGCAAAATCTTTGAGCGCGCGCAATTC 988

RESULT 2
PCT-US02-27884-5525
Sequence 5525, Application PC/TUS0227884
GENERAL INFORMATION:
APPLICANT: The Dow Chemical Company
APPLICANT: Dow Agro Sciences, LLC
TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Character
FILE REFERENCE: DOW-07611
CURRENT APPLICATION NUMBER: PCT/US02/27884
NUMBER OF SEQ ID NOS: 7560
SOFTWARE: PatentIn version 3.1

Query Match 49.6%; Score 490.2; DB 1; Length 623;
Best Local Similarity 89.6%; Pred. No. 5e-111;
Matches 560; Conservative 0; Mismatches 38; Indels 27; Gaps 2;

QY CTCTATATATACCATGGCTTTTGCAGACACACAGAAATGATGGCATGTGACAAAGAC 146
DB 1 CTCTATATATACCATGGCTTTTGCAGACACACAGAAATGATGGCATGTGACAAAGAC 60
QY 147 TGTCTATCTGTGTGACAAATTAAGTACAGATTAAGATATATATATATATATATAT 206
DB 61 TGTCTATCTGTGTGACAAATTAAGTACAGATTAAGATATATATATATATATATAT 120
QY 207 ATGCCATCAGTCGCAAGGCACTGTCAAGCTTGGCACTACATATCTTTTGGAGAGTTCT 266
DB 121 ATGCCATCAGTCGCAAGGCACTGTCAAGCTTGGCACTACATATCTTTTGGAGAGTTCT 180
QY 267 ATACTGTAGACACACTTTTGTATCAGCTCTTCAACCAAACTGGAGTTGGATTAAGCTT 326
DB 181 ATACTGTAGACACACTTTTGTATCAGCTCTTCAACCAAACTGGAGTTGGATTAAGCTT 240
QY 327 TGAAGGTACACCAAAAAATGTGAAGCCACAGAAACCCATTTGACAGTGAAGAACCAAGT 386
DB 241 TGA-----AGAAACCATTTGACACTGAGAAACCAAGT 274
QY 387 AGCCAAAGTGACAGCATGTTTGTGTGAACAAGAGAAATGTTTGGCTGCAAGAAAC 446
DB 275 AGCTAAAGTGACAGCATGTTTGTGTGAACAAGAGAAATGTTTGGCTGCAAGAAAC 334
QY 447 TGTCTACCAACAGAAAGATATGAGCAATGGCAGGCAATGAGCTCTTCA 506
DB 335 TGTCTACCAACAGAAAGATATGAGCAATGGCAGGCAATGAGCTCTTCA 394
QY 507 ATGACGACGAGAGCTGTGTATATAGCCCTTCCACTATACCGACATGAGGGGCGCTT 566
DB 395 ATGACGACGAGAGCTGTGTATATAGCCCTTCCACTATACCGACATGAGGGGCGCTT 454
QY 567 ATATGTAAACATCACCATTATTCACCTTATCAGAGAGAGGCACTTAAAGCAAGTTGA 626
DB 455 CTACTGTAAACATCACCATTATTCACCTTATCAGAGAGAGGCACTTAAAGCAAGTTGA 514
QY 627 GGGTGACCATGAATTAATTCACAGACACAGAGATTACTCAGATCATACAGC 686
DB 515 GGGTGACCATGAATTAATTCACAGACACAGAGATTACTCAGATCATACAGC 573
QY 687 CGACCAAGTTGATGATCTTATCT 711
DB 574 CGACCAAGTTGATGATCTTATCT 598

RESULT 5
US-09-705-926-4708/c
; Sequence 4708, Application US/09705926
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingtong
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15481A)
; CURRENT APPLICATION NUMBER: US/09/705,926
; CURRENT FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 21634
; SEQ ID NO 4708
; LENGTH: 734
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-705-926-4708

Query Match 40.6%; Score 401.2; DB 28; Length 734;
Best Local Similarity 81.1%; Pred. No. 6.9e-89;
Matches 482; Conservative 0; Mismatches 103; Indels 9; Gaps 1;

QY 71 TTTTCTGTAAACTGTGCTATATATAGCATGGCTTTTGCAGACACACAGAAATGCA 130
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DB 733 TTTTCTGTAAACTGTGCTATATATAGCATGGCTTTTGCAGACACACAGAAATGTA 674
QY 131 TGGCATGTGACAGACTGTCTATCTGTTGCAAAATTAAGTACAGATTAAGAAATCTATC 190
DB 673 TGGCATGTGACAGACTGTCTATCTGTTGCAAAATTAAGTACAGATTAAGAAATCTATC 614
QY 191 ACAAGCTTTGTTGAGATGCCATCATGCAAGGCACTGTCAAGCTTTGGCAACTACATAT 250
DB 613 ATAAAGCTTTGTTGAGATGCCATCATGCAAGGCACTGTCAAGCTTTGGCAACTACATAT 554
QY 251 CCTTGGAGGAGTCTTATGCTAGACACACTTGTATGAGCTCTTCAACCAACTGCA 310
DB 553 CATTTGAGGAGTCTTATGCTAGACACACTTGTATGAGCTCTTCAACCAACTGCA 494
QY 311 GTTTGATTAAGCTTTGAAAGTACACCAAAATGTAAGCCACAGAAACCATTTGACA 370
DB 493 GTTTGATTAAGCTTTGAAAGTACACCAAAATTTGTAAGCCAGAAATGTAAGCTTTGACA 443
QY 371 GTGAAACACAGAGTACCAAGTGAACAGATGTTTGGTGAAGAGAGAGAAATGTT 430
DB 442 ATGAGAAACACAGATGTCGCAAAAGTTTCAAGCATGTTTGGTAAGTGAAGGAGAAATGTT 383
QY 431 TTGGCTGCAAGAAACCTGTCTAACCCACAGAAAGATGACCAATGGCAGGCAATAC 490
DB 382 TTGGCTGCAAGAAACCTGTCTAACCCACAGAAAGATGACCAATGGCAGGCAATAC 323
QY 491 ATAGAGCTGCTTCCATGACAGCCAGGAGCTGTGTAATAGCCCTTCCACTATACCG 550
DB 322 ACAAAATTTGCTTCAATATGATGATCATGAGGCTGTGTAATTAAGCCATTCACATATTTG 263
QY 551 CACATGAGGGGCGCTTATATTTGTAACATCACCATTATTCACCTTATTCAGAGAGAGGCA 610
DB 262 CTCAGAGGGGCGCTTATATTTGTAACATCACCATTATTCACCTTATTCAGAGAGAGGCA 203
QY 611 ACTTAACAGCTTGAAGGTGACCATTAATTAATTCAGACACACAGAGAG 664
DB 202 ACTTAACAGCTTGAAGGTGACCATTAATTAATTCAGACACACAGAGAG 149

RESULT 6
PCT-US02-27884-3350
; Sequence 3350, Application PC/TUS0227884
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Confering Altered Metabolic Character
; FILE REFERENCE: DOW-07611
; CURRENT APPLICATION NUMBER: PCT/US02/27884
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3350
; LENGTH: 632
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27884-3350

Query Match 39.0%; Score 385.8; DB 1; Length 632;
Best Local Similarity 83.4%; Pred. No. 4.4e-85;
Matches 466; Conservative 0; Mismatches 82; Indels 11; Gaps 2;

QY 98 CCATGGCTTTTGCAGACACACAGAAATGATGGCATGTGACAGTCTATCTG 157
DB 85 CAATGGCATTTGCAAGACACACAGAAATGATGGCA--TGAAGAGACAGTATCTAG 142
QY 158 TTGACAAATTAAGTACAGATTAAGATATATCAAGCAAGCTTTTGCAGATGCACTACT 217
DB 143 TTGATTAATTAAGTACAGATTAAGATATATCAAGCTTTTGCAGATGCACTACT 202
QY 218 GCAAGGCACTGTCAAGCTTTGCACTACATATCTTTGAGGAGATTTCTATATCTGAGAC 277
||||| |

Db	203	GCAGGGTACTCTCAGGTTAGCAACTACATTAATTATTGGAGGAGTTCTCTATTATTAGAC	262
OY	278	CACACTTTGATCAGCTCTTCAACAAACTGGCAGTTTGGATTAAGAAGGTACAC	337
Db	263	CTCACTTTGATCAGCTCTTTTAAAGAAGTGGAGTGTGGACAAAGCTTTGAAGGGGAC	322
OY	338	CAAAAAATGTAACCCACAGAAACCCATTGCAGTGGAAAAACCAAGGTAGCCAAAGTGA	397
Db	323	CCAAAATTTGTAAACCCAGAGAAA-----GATGGAAAAACCAACAGCTGTAAAGTCT	373
OY	398	CAAGCATTTTGGTGGAAACAAGAGAAATTTTGGCTGCAAGAAACGTGTACACAA	457
Db	374	CAAGATTTTGGTGGAAACAAGGAGAAATTTTGGCTGCAAGAAATCTGTATATCCA	433
OY	458	CAGAAAAGGTATCAGCCCAANTGGACGCCCATACCTAAGAGCTGCTTCAATGCAGCCAG	517
Db	434	CAGAAAAGGTATCAGTGAATGGAACACCATATTCACAAACCTGCTTCAATTAAGTACATG	493
OY	518	GAGGCTGTATTAAGCCCTTCACAACTATACCCGACATGAGGGGGGCGCTTATATTGTAAC	577
Db	494	GTTGATGCACAATTAGCCCATTCACACTATATTGTGGCAGAGGGGGCGCTTTACTGCAAAC	553
OY	578	ATCACCATTTTCAACTTATATCAAGGAGAAGGCACTTAAGCAAGCTTGAGGGGTACATG	637
Db	554	ATCACCATTTTCAACTATATCAAGGAGAAGGAAGCACTTAAGCCAGCTTGAGGGGTATCATG	613
OY	638	AAATGAATTCACAGCAAC 656	
Db	614	ACAAGAAATACAGTATGAAC 632	

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RESULT 7
US-09-705-926-3115
: Sequence 3115, Application US/09705926
: GENERAL INFORMATION:
: APPLICANT: Kovalic, David K.
: APPLICANT: Liu, Jingdong
: APPLICANT: Wiegand, Roger C.
: TITLE OF INVENTION: ANNOTATED PLANT GENES
: FILE REFERENCE: 38-21(15481)A
: CURRENT APPLICATION NUMBER: US/09/705,926
: CURRENT FILING DATE: 2000-11-06
: NUMBER OF SEQ ID NOS: 21634
: SEQ ID NO 3115
: LENGTH: 618
: TYPE: DNA
: ORGANISM: Lycopersicon esculentum
US-09-705-926-3115

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Query Match	37.68;	Score 371.6;	DB 28;	Length 618;
Best Local Similarity	89.28;	Pred. No. 1.5e-81;		
Matches 423; Conservative	0;	Mismatches 49;	Indels 2;	Gaps 2

Qy	93	TATGGCATTGGCTTTTGGAGGAAACACAGAATGGATGGCAATGACAAAGACTGCTA	1522
Db	144	TATACCAATGGCATTTTGGAGGAACAACCAAAAGTGGATGGCTTGTATCAAGAAGCTGCTTA	2030
Qy	153	TCTGGTTACCAATTTAACTGCAGATTAACAGAAATGTATCACAAAGCTGTTTTCAGATCCCA	2122
Db	204	TCTGGCTGACAGGTTTAACTGTCAGATTAACAGAAATGTATCACAAAGCTGTTTGGATGTCA	2652
Qy	213	TCACCTGCAAGGGCACACTGTCAAGCTTGGCACTACAAATTCCTTTGAGGAGTTCTATACGTG	2727
Db	264	TCACGCAAGGGCAACCCCTCAAGCTTGGCACTACAAATTCCTTTGAAAGAGACTCTGTACTCG	3233
Qy	273	TAGACACACA -CTTTGATGAGCTCTTCAAAACAAACTGGCAGTTTGGATAAAAGCTTTAAG	3311
Db	324	TAGACACACACTTTTGATGAGCTCTTCAAAACAAACTGGCAGCTTGGATAAAAGCTTTTGAAG	3633
Qy	332	GTACACCAAAAAATGTGAAGCCACAGAAAACCCATTGACAGTGAGAAACCA -CAGGTAGCC	3900
Db	384	GGACACCAAAAAATTTGTGAAGCCACAGAAAGCTCATTTGACAGTGAGAAACCAACAGGTGTGCT	4438

OY	391	AAAGTGACAGCATGTTTGGTGGGAACAAGAGAGAATGTTTGGCTGCAAGAAACAGTGC	450
Db	444	AAAGGACACAGATGTTGGTGGAAACAAGGAGAAATGTTTGGCTCCGAACACAGTGC	503
OY	451	TACCCACAGAAAAGGTATCAGCCAAATGGACGCCATATCCATTAAGAGCTGCTTCCAATGC	510
Db	504	TATCCACAGAAAAGGTATCAGTTAAATGGTACACCAATACACAAAACACTCTTCCAATGT	563
OY	511	AGCCACGAGAGCTGTGTATATTAAGCCCTTCCACATATACCGACATAGAGGGGCGC	564
Db	564	AGCCATGGAGGGGGGTGTAATTAAGCTCTTCCACCTCTATGCGACATGGAAGGGGGC	617

RESULT 8
US-10-155-881-36087
; Sequence 36087, Application US/10155881

```

1  APPLICANT: Dootson, Stanton B.
2  APPLICANT: Kovalic, David K.
3  APPLICANT: Liu, Jindong
4  APPLICANT: Lutfiyya, Linda L.
5  APPLICANT: McIninch, James
6  TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
7  TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
8  FILE REFERENCE: 38-21(15300)J
9  CURRENT APPLICATION NUMBER: US/10/155,881
10 CURRENT FILING DATE: 2002-05-22
11 NUMBER OF SEQ ID NOS: 37595
12 SEQ ID NO 36087
13 LENGTH: 994
14 TYPE: DNA
15 ORGANISM: Glycine max
16 US-10-155-881-36087

```

Query Match	34.8%;	Score 343.4;	DB 41;	Length 994;
Best Local Similarity	77.6%;	Pred. No. 1.7e-74;		
Matches 429;	Conservative 0;	Mismatches 121;	Indels 3;	Gaps 1

QY	100	ATGCGTTTGGAGGAGCCACAGAAAATGCAATGTCATGTGCAAGACTGTCATGCTT	159
Db	164	ATGCGATTTTGCAGAGACACACAGAGATGTATGCGCTGTGCAAAACCGTTTATCTG	223
QY	160	GACAAATTAAGTCAGATTAACAGATCTATCCAAAGCTGTTCAGANTGCCATCACTG	219
Db	224	GATTAAGTGACCGCGGATTAACCCGAGTTTCCACAAGCTTGCTCAATGCCATCACTG	283
QY	220	AAGGCACTGTCAAGCTTGGCAACTACAAATTCCTTTGAGGAGGTTCTATCTAGAGCA	279
Db	284	AAAGSAAACCTCAAGCTGAGCACTACCAACTTTTGAAGGAGTTCTTATTTAGAACCA	343
QY	280	CACATTGATCAGCTCTTAAACAACTGCGAGTTTGGATTAAGACTTTGAAGTACCA	339
Db	344	CACTTTGAACCAAGTCTCAAAAGAAACAGGAGCCTTGACAAAGCTTTGAAGGAACCA	403
QY	340	AAAAATGTGAAGCCACAGAAACCATTGACAGTGAAGAAACACAGTAGCCAAAGTACA	399
Db	404	AAAAATGGCAAGCCACAGAAATTTTGA---AAGAGAACTGTGAGAGCCAAAGTCTCA	460
QY	400	AGCATGTTTGGTGCAACAGAGAGAAATGTTGGTGCAGAGAAATGTCATACCACAA	459
Db	461	AGTATGTTTGGAGGAACAGGAGCAAAATGTCGTGTGTTGTGCAAAACGGTTTATCCACT	520
QY	460	GAAAAGTATCAGCCAAATGSCACGCGCATACATTAAGAGCTGCTTCAAATGACGCACGA	519
Db	521	GAGAAAGGTGACGTGTAAGGAACCCCTTACCATTAAGAGTGTTCCTCAATGCTGCATGGA	580
QY	520	GCGCTGTGAATAGCCCTCCCAACTATCCGCACATGAGGGGCGCTTATATTTGAACAT	579
Db	581	GGGTGTGTTATCAGTCTCTTCCAAATTACTATGACACACGAGGGAACCAACTCTACTGCAACAC	640
QY	580	CACCATATTTCAACTTATCAAGAGAGGCGCACTTAAAGCAAGCTTTGAGGGTGACCATGAA	639
Db	641	CACCATGTGCATATGATCAAGAGAGGCGCAATTTAAGCCAACTTGAAGGTGACCAATAG	700


```
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15300)J
; CURRENT APPLICATION NUMBER: US/10/155,881
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 37595
; SEQ ID NO 36088
; LENGTH: 973
; TYPE: DNA
; ORGANISM: Glycine max
US-10-155-881-36088

Query Match
Best Local Similarity 34.4%; Score 339.6; DB 41; Length 973;
Matches 439; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 100 ATGGCTTTTGCAGGAGACACAGAAATGCATGCGATGTGACAGAGCTGTCTATCTGTT 159
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 166 ATGGCATTTTGCAGGAGAACCCAGAGTGTATGGCTGCGACAAACGGTTTATCTGTT 225
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 160 GACAAATTACTGACAGATACAGAAATCTATCACAAAGCTTTGTTGAGTGCATCTGC 219
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 226 GATTAAGTTACCGCGGATTAACCGAGTGTTCACAAAGCTTGTTCAGATGCCATCTGC 285
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 220 AAGGCACTGTCAAGCTTGACATTCCTTTGAGGAGTTCTATACCTGTACCA 279
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 286 AAGGAACCCCTCAGCTGACATCTCTTTGAGGAGTTCTTTACTGCAAGCCA 345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 280 CACTTGTATCAGCTTCTTCAACAACTGCGAGTTTGATTAAGCTTTGAGGTACACA 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 346 CATTTTGACCACTGTCTTCAAAAGATGGAGCCTTGACAAAGCTTTGAGGACACCA 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 340 AAAAATGTAGAGCCAGAAACCCATTGACAGTGAAGAACACAGGTAGCCAAAGTGACA 399
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 406 AAAATTGCCAAGCAGAAATAATTTTGA--AGAGAAACCTGACAGCCAAAGCTCTCA 462
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 400 AGCATGTTGGTGAGACAGAGAAATGTTTGGCTGCAAGAAACCTGCTACCCACA 459
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 463 AGTATGTTGGTGAGAACAGGAAATGTCGTGTTGACAAACGGGTATCTCCACT 522
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 460 GAAAGGTATCAGCCATATGGACGCCATACATTAAGAGCTGCTTCCATGACGACGCA 519
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 523 GAGAAGTACTGTGATGGAATGGAATCTTACATTAAGAGTGTTTAAATGCTGCCATGCA 582
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 520 GGCTGTGTAATAAGCCCTTCCAACTATACCGCATATGAGGGGCGCTTATATGTAACAAT 579
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 583 GGGTGTGTTATCAGTCTCTTCCAACTATACGACACAGAGGAAACCTTACTSCAAACAC 642
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 580 CACCATATTCACATTAACAAGGAGGCACTTAAGCAAGCTTGAAGGTGACCATGAA 639
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 643 CACCATGTCCAAATGATGAGGAGGCAATTAACCAACTTGAAGGTGACCATGAG 702
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 640 ATGAATTCACGACAAACAGAGAGTTACTGCAGAGTCATACACAG 685
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 703 AAGAGTGCAGCTAATGGAATAATCAATGATGGAAGAGTTTCCGACAG 748
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-60-312-544-1609
; Sequence 1609, Application US/60312544
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerlon, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
```

```
; FILE REFERENCE: 38-10(52726)A
; CURRENT APPLICATION NUMBER: US/60/312,544
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 10730
; SEQ ID NO 1609
; LENGTH: 973
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(756)
; OTHER INFORMATION: Clone ID: 700888137_FLI
US-60-312-544-1609

Query Match
Best Local Similarity 34.4%; Score 339.6; DB 75; Length 973;
Matches 439; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 100 ATGGCTTTTGCAGGAGACACACAGAAATGCATGCGATGTGACAGAGCTGTCTATCTGTT 159
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 166 ATGGCATTTTGCAGGAGAACCCAGAGTGTATGGCTGCGACAAACGGTTTATCTGTT 225
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 160 GACAAATTACTGACAGATACAGAAATCTATCACAAAGCTTTGTTGAGTGCATCTGC 219
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 226 GATTAAGTTACCGCGGATTAACCGAGTGTTCACAAAGCTTGTTCAGATGCCATCTGC 285
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 220 AAGGCACTGTCAAGCTTGACATTCCTTTGAGGAGTTCTATACCTGTACCA 279
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 286 AAGGAACCCCTCAGCTGACATCTCTTTGAGGAGTTCTTTACTGCAAGCCA 345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 280 CACTTGTATCAGCTTCTTCAACAACTGCGAGTTTGATTAAGCTTTGAGGTACACA 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 346 CATTTTGACCACTGTCTTCAAAAGATGGAGCCTTGACAAAGCTTTGAGGACACCA 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 340 AAAAATGTAGAGCCAGAAACCCATTGACAGTGAAGAACACAGGTAGCCAAAGTGACA 399
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 406 AAAATTGCCAAGCAGAAATAATTTTGA--AGAGAAACCTGACAGCCAAAGCTCTCA 462
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 400 AGCATGTTGGTGAGACAGAGAAATGTTTGGCTGCAAGAAACCTGCTACCCACA 459
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 463 AGTATGTTGGTGAGAACAGGAAATGTCGTGTTGACAAACGGGTATCTCCACT 522
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 460 GAAAGGTATCAGCCATATGGACGCCATACATTAAGAGCTGCTTCCATGACGACGCA 519
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 523 GAGAAGTACTGTGATGGAATGGAATCTTACATTAAGAGTGTTTAAATGCTGCCATGCA 582
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 520 GGCTGTGTAATAAGCCCTTCCAACTATACCGCATATGAGGGGCGCTTATATGTAACAAT 579
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 583 GGGTGTGTTATCAGTCTCTTCCAACTATACGACACAGAGGAAACCTTACTSCAAACAC 642
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 580 CACCATATTCACATTAACAAGGAGGCACTTAAGCAAGCTTGAAGGTGACCATGAA 639
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 643 CACCATGTCCAAATGATGAGGAGGCAATTAACCAACTTGAAGGTGACCATGAG 702
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 640 ATGAATTCACGACAAACAGAGAGTTACTGCAGAGTCATACACAG 685
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 703 AAGAGTGCAGCTAATGGAATAATCAATGATGGAAGAGTTTCCGACAG 748
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-09-654-617-2276
; Sequence 2276, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 2276
; LENGTH: 1006
; TYPE: DNA
```


ORGANISM: Glycine max
US-09-654-617-2276

Query Match 34.3%; Score 338.6; DB 25; Length 1006;
Best Local Similarity 77.0%; Pred. No. 2.7e-73;
Matches 426; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 100 ATGGCTTTTGCAGAGACACAGAGAAATGATGAGCATGTGCAAGACTGTCTATCTGTT 159
DB 176 ATGGCTTTTGCAGAGACACAGAGAAATGATGAGCATGTGCAAGACTGTCTATCTGTT 235
QY 160 GACAAATTAATGATGATTAACAGATATATCACAACCTGTTTCAATGCGATCACTGC 219
DB 236 GATTAAGTTGACCGGGATTAACCGGATTTTCCACAACCTGTTTCAATGCGATCACTGC 295
QY 220 AAGGCACTGTGACCTTGGCAACTATCAATTCCTTTGAGGAGTTCTATCTGATAGACA 279
DB 296 AAGGAACCTCTCAAGCTGAGCACTACACTCTTTTGAAGGAGTTCTTTACTGACGCGCA 355
QY 280 CACTTTGATGAGCTCTTCAAAACAACTGGCAGTTTGATTAAGCTTTGAAGGTACACA 339
DB 356 CACTTTGACCACTGTTCAAAAGAACTGTGATCTTGACAAACCTTCGAAGGACACCA 415
QY 340 AAAAATGTGAAGCCACAGAAACCATTTGACAGTGAAGAAACACAGTGAAGCACTACA 399
DB 416 AAAATGTGTAACCCAGAAAAAACCGGGGA--AGAGAAACCTGCAGCAACCAAGTCTCA 472
QY 400 AGCATGTTTGTGGGAACAGAGAAATGTTTGGCTGCAAGAAACCTGTCTACCCANCA 459
DB 473 AGTATGTTTGTGGGAACAGATTAATGTGCCGGTGTGAGAAACAGTGTATCCACT 532
QY 460 GAAAAGTATACCCAAATGCGACCATTAACATTAAGAGCTGCTTCAATGCAAGCAGCA 519
DB 533 GAAAAGTATACCTGTGAATGGAACCTCTTATCACAAGAGTTGTTCAATGCACTCATGA 592
QY 520 GCGTGTATTAAGCCCTTCAACTATACCGCATAGAGGGGCGCTTATATGTAACAT 579
DB 593 GGGGTGTTTATTAAGTCCCACTACATTCACAGAGGCAAACTCTACTCGCAAGCAC 652
QY 580 CACCATTATCACTTATCAAGAGAGGAGGCACTTAAGCAAGCTTGAGGTGACATGAA 639
DB 653 CACCAGTCCCACTGATCAAGAGAGGCAATTTAAGCAACTTGAACGTGACAAATGAG 712
QY 640 ATGAATTCACGA 652
DB 713 AAGAGTCAACTA 725

RESULT 14
US-09-684-016-2276
Sequence 2276, Application US/09684016
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 38-21(15097)D
CURRENT APPLICATION NUMBER: US/09/684, 016
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/654, 617
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 2276
LENGTH: 1006
TYPE: DNA
ORGANISM: Glycine max
US-09-684-016-2276

Query Match 34.3%; Score 338.6; DB 27; Length 1006;
Best Local Similarity 77.0%; Pred. No. 2.7e-73;
Matches 426; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 100 ATGGCTTTTGCAGAGACACAGAAATGATGAGCATGTGACAAAGCTGTCTATCTGTT 159
DB 176 ATGGCTTTTGCAGAGACACAGAAATGATGAGCATGTGACAAAGCTGTCTATCTGTT 235

DB 176 ATGGCTTTTGCAGAGACACAGAAATGATGAGCATGTGACAAAGCTGTCTATCTGTT 235
QY 160 GACAAATTAATGATGATTAACAGATATATCACAACCTGTTTCAATGCGATCACTGC 219
DB 236 GATTAAGTTGACCGGGATTAACCGGATTTTCCACAACCTGTTTCAATGCGATCACTGC 295
QY 220 AAGGCACTGTGACCTTGGCAACTATCAATTCCTTTGAGGAGTTCTATCTGATAGACA 279
DB 296 AAGGAACCTCTCAAGCTGAGCACTACACTCTTTTGAAGGAGTTCTTTACTGACGCGCA 355
QY 280 CACTTTGATGAGCTCTTCAAAACAACTGGCAGTTTGATTAAGCTTTGAAGGTACACA 339
DB 356 CACTTTGACCACTGTTCAAAAGAACTGTGATCTTGACAAACCTTCGAAGGACACCA 415
QY 340 AAAAATGTGAAGCCACAGAAACCATTTGACAGTGAAGAAACACAGTGAAGCACTACA 399
DB 416 AAAATGTGTAACCCAGAAAAAACCGGGGA--AGAGAAACCTGCAGCAACCAAGTCTCA 472
QY 400 AGCATGTTTGTGGGAACAGAGAAATGTTTGGCTGCAAGAAACCTGTCTACCCANCA 459
DB 473 AGTATGTTTGTGGGAACAGATTAATGTGCCGGTGTGAGAAACAGTGTATCCACT 532
QY 460 GAAAAGTATACCCAAATGCGACCATTAACATTAAGAGCTGCTTCAATGCAAGCAGCA 519
DB 533 GAAAAGTATACCTGTGAATGGAACCTCTTATCACAAGAGTTGTTCAATGCACTCATGA 592
QY 520 GCGTGTATTAAGCCCTTCAACTATACCGCATAGAGGGGCGCTTATATGTAACAT 579
DB 593 GGGGTGTTTATTAAGTCCCTCACTACATTCACAGAGGCAAACTCTACTCGCAAGCAC 652
QY 580 CACCATTATCACTTATCAAGAGAGGAGGCACTTAAGCAAGCTTGAGGTGACATGAA 639
DB 653 CACCAGTCCCACTGATCAAGAGAGGCAATTTAAGCAACTTGAAGGTGACAAATGAG 712
QY 640 ATGAATTCACGA 652
DB 713 AAGAGTCAACTA 725

RESULT 15
US-09-733-089-12353
Sequence 12353, Application US/09733089
GENERAL INFORMATION:
APPLICANT: Dotson, Stanton B.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
APPLICANT: Lutfiyya, Linda L.
APPLICANT: McIninch, James
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-21(15300)D
CURRENT APPLICATION NUMBER: US/09/733, 089
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/474, 435
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 09/654, 617
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 09/620, 392
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 24143
SEQ ID NO 12353
LENGTH: 1006
TYPE: DNA
ORGANISM: Glycine max
US-09-733-089-12353

Query Match 34.3%; Score 338.6; DB 29; Length 1006;
Best Local Similarity 77.0%; Pred. No. 2.7e-73;
Matches 426; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 100 ATGGCTTTTGCAGAGACACAGAAATGATGAGCATGTGACAAAGCTGTCTATCTGTT 159
DB 176 ATGGCTTTTGCAGAGACACAGAAATGATGAGCATGTGACAAAGCTGTCTATCTGTT 235


```
Db 176 ATGCGATTTCAGAGAACACAGAAAGTGTATGCCCTGTGACAAAACCGTTATCTGTT 235
QY 160 GACCAATTAACTGCAGATTAACAGAACTATATCACAAAGCTTTGTTTCAGATGCCATCATGCG 219
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 236 GATTAAGTTGACCGGATTAACCGATTTTCACAAAAGCTTGCTTCAGATGCCATCATGCG 295
QY 220 AAGGCACTGTCAAGCTTGGCACTTACATCTTGTGAGGAGTTCTATCTGTAGACCA 279
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 296 AAAGGACCCCTCAAGCTGAGCACTACAACTCTTTGAGGAGTTCTTACTGCAAGGCCA 355
QY 280 CACTTGTATCAGCTCTTCAAAACAACTGGCAGTTTGGATAAAAGCTTTGAAGGTACACCA 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 356 CACTTGTGACCACTGTTCAAAAGAACTGTGTCTTGTGACAAAAGCTTGCAGAGGACACCA 415
QY 340 AAAAATGTGAAGCCACAGAAACCCATTGACAGTGAAGAAACACAGGTAGCCAAAGTGACA 399
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 416 AAAATTGTAAACCAAGAAAACCGGGGA--AGAGAAACCTGCAGCAACCAAAAGTCTCA 472
QY 400 AGCATGTTTGGTGAACAAGAGAATGTTTGGCTGCAAGAAAAGTGTCTACCCACA 459
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 473 AGTATGTTTGGTGAAGTGAAGATTAATGTGCCGGTTGTCAAGAAAACAGTGTATCCCACT 532
QY 460 GAAAAGTATCAGCAATGGCAGGCATACATTAAGAGCTGCTCCATGCAAGCCACGGA 519
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 533 GAAAAGTTACTGTGATGGAAGCTCTTATCAAGAAGTTGTTCAATGCACTCATGGA 592
QY 520 GGCTGTGTAATAGCCCTTCACACTATACCGCACATGAGGGCGCTTATATTGTAAACAT 579
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 593 GGGTGTGTTATTAAGTCCCTCCAACTACATTGCACAGAGGGCAAACTCTACTGCCAAGCAC 652
QY 580 CACCATATTCAACTTATCAAGGAGAGGCAACTTAAGCAAGCTTGAGGGTGAACCATGAA 639
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 653 CACCAAGTCCCAAGTGAAGGAGAGGCAATTAAAGCAACTTGAAGTGAAGTGCACATGAG 712
QY 640 ATGAATTCACGA 652
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 713 AAGAGTGCACTTA 725
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Search completed: November 23, 2002, 00:30:07
Job time : 3191 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2002, 22:18:28 ; Search time 61 Seconds

(without alignments)
6967.572 Million cell updates/sec

Title: US-09-928-412-1

Perfect score: 988

Sequence: 1 gaatcgcgcgcctcccaaa.....ctttagcgcgcgaattc 988

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280232 seqs, 215092063 residues

Total number of hits satisfying chosen parameters: 560464

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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2: /cgn2_6/prodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/prodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/prodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/prodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/prodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	179.8	18.2	861	US-10-278-173-83	Sequence 83, Appl
2	75	7.6	504	US-10-152-319A-579	Sequence 579, Appl
3	44.4	4.5	853	US-10-152-319A-2070	Sequence 2070, Ap
4	42.2	4.3	9515	US-10-240-453-182	Sequence 182, App
5	40.4	4.1	294	US-09-724-676-43076	Sequence 43076, A
6	40.4	4.1	334	US-09-724-676-43075	Sequence 43075, A
7	40.4	4.1	730	US-09-724-676-43072	Sequence 43072, A
8	40.4	4.1	732	US-09-724-676-43074	Sequence 43074, A
9	40.4	4.1	875	US-09-724-676-43071	Sequence 43071, A
10	40.4	4.1	877	US-09-724-676-43069	Sequence 43069, A
11	40.4	4.1	1141	US-09-724-676-43068	Sequence 43068, A
12	40.4	4.1	1165	US-09-724-676-43067	Sequence 43067, A
13	39.6	4.0	466	US-09-724-676-43065	Sequence 43065, A
14	39.6	4.0	506	US-09-724-676-43059	Sequence 43059, A
15	39.6	4.0	902	US-09-724-676-43064	Sequence 43064, A
16	39.6	4.0	904	US-09-724-676-43066	Sequence 43066, A
17	39.6	4.0	1047	US-09-724-676-43063	Sequence 43063, A
18	39.6	4.0	1049	US-09-724-676-43065	Sequence 43065, A
19	39.6	4.0	1337	US-10-240-453-306	Sequence 306, App
20	39.6	4.0	11812	US-10-240-453-7	Sequence 7, Appl1
21	39.4	4.0	12409	US-10-240-485-164	Sequence 164, App
22	39	3.9	20486	US-10-257-166-174	Sequence 174, App
23	38.6	3.9	9728	US-10-240-485-31	Sequence 31, Appl
24	38.4	3.9	6121	US-10-240-453-11	Sequence 11, Appl
25	38.2	3.9	6391	US-10-240-453-37	Sequence 37, Appl
26	38	3.8	17848	US-10-240-453-37	Sequence 37, Appl

27	38	3.8	17848	6	US-10-257-166-57	Sequence 57, Appl
28	37.6	3.8	1218	6	US-10-092-411A-2422	Sequence 2422, Ap
29	37.4	3.8	14924	6	US-10-240-452-21	Sequence 21, Appl
30	36.8	3.7	5544	6	US-10-240-485-174	Sequence 174, App
31	36.8	3.7	6298	6	US-10-240-453-67	Sequence 67, Appl
32	36.8	3.7	7025	6	US-10-240-453-46	Sequence 46, Appl
33	36.8	3.7	7025	6	US-10-257-166-142	Sequence 142, App
34	36.8	3.7	8866	6	US-10-240-453-154	Sequence 154, App
35	36.8	3.7	15479	6	US-10-257-166-45	Sequence 45, Appl
36	36.6	3.7	11996	6	US-10-240-166-45	Sequence 45, Appl
37	36.6	3.7	13123	6	US-10-240-452-64	Sequence 64, Appl
38	36.4	3.7	387	5	US-09-513-999C-1611	Sequence 1611, Ap
39	36.4	3.7	482	5	US-09-513-999C-11929	Sequence 11929, A
40	36.4	3.7	754	5	US-09-724-676-13712	Sequence 13712, A
41	36.4	3.7	904	5	US-09-724-676-13711	Sequence 13711, A
42	36.4	3.7	6018	6	US-10-240-453-103	Sequence 103, App
43	36.4	3.7	10467	6	US-10-240-453-328	Sequence 328, App
44	36.4	3.7	14551	6	US-10-240-485-137	Sequence 137, App
45	36	3.6	284	5	US-09-513-999C-27884	Sequence 27884, A

ALIGNMENTS

```
RESULT 1
US-10-278-173-83
: Sequence 83, Application US/10278173
: GENERAL INFORMATION:
: APPLICANT: Jiang, Cai-Zhong
: APPLICANT: Brown, Pierre
: APPLICANT: Riechmann, Jose-Luis
: APPLICANT: Pineda, Omaira
: APPLICANT: Zhang, James
: APPLICANT: Yu, Guo-Liang
: APPLICANT: Pillgrim, Marsha
: APPLICANT: Reddie, James
: APPLICANT: Heard, Jacqueline
: APPLICANT: Reuber, Lynne
: APPLICANT: Ratcliffe, Oliver
: APPLICANT: Adam, Luc
: APPLICANT: Samaha, Raymond
: TITLE OF INVENTION: POLYNUCLEOTIDES FOR ROOT TRAIT ALTERATION
: FILE REFERENCE: M81-009
: CURRENT APPLICATION NUMBER: US/10/278,173
: CURRENT FILING DATE: 2002-10-21
: PRIOR APPLICATION NUMBER: US/09/533,392
: PRIOR FILING DATE: 2000-03-22
: PRIOR APPLICATION NUMBER: 60/125,814
: NUMBER OF SEQ ID NOS: 177
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 83
: LENGTH: 861
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
: FEATURE:
: OTHER INFORMATION: G654
US-10-278-173-83

Query Match      18.2%   Score 179.8;   DB 6;   Length 861;
Best Local Similarity 58.6%   Pred. No. 4.2e-41;
Matches 352;   Conservative 0;   Mismatches 242;   Indels 7;   Gaps 2;

OY 100 ATGGCTTTGACGAGACACACAGCAATGATGCGATGTCAGATGCTGTATCTGTT 159
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 76 ATGCTTTTACAGAACATCTCAACAGAAATGCAAGGCTTGTGAAGACTGTTATGCTGT 135
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 160 GACAAATTAACCTGACGATTAACAGATCTATCAACAGCTGTTTCAGATGCCATCTGC 219
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 136 GAGCTTCTCTGCTGATGAGCTTGAATATCAACAGCTTGTCAATATCACTACCTGC 195
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 220 AAGGCACTGTCAAGCTTGCACTACATATCTTTAGGAGGATTCATATCTAGACCA 279
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 196 AAAACGAGGCTTCAGCTGAGTAGTTCATCATGGAAGTGTGTTTGTACTGTAAAGCT 255
QY 280 CACTTGTGATCAGCTTCTTAACAACACTGGCAGTTGGATTAAGCTTTGAAGGTACACCA 339
Db 256 CATTGTGAGCAGCTCTTTAAGGAGAGTGTGTGTTCACACGAACCTTTCAGTCACTGCA 315
QY 340 AAAAATGTGAAGCCAGAAACCCATTGACAGTGAAGAAACCCAGAGTACCCAAATGTACA 399
Db 316 AAA-----TGGCTGACAAATCACTCTGAGCTGACAGAGAGCCCTAGCCGAGTGTCT 369
QY 400 AGCATGTTTGTGGAACAAGAGAGAAATGTTTGGCTCAAGAAACCTGTACCAACA 459
Db 370 GGCAGGTTCTCTGTCGACACAGAGAAATGCGGCACTTGTAGTAAACCTGTATCTTAT 429
QY 460 GAAAAGTATCAAGCCATGACAGCCATACATTAAGAGCTGCTTCCAAATGACAGCCGGA 519
Db 430 GAAAAGGTACAGTGCAGAGCAGACATATCACAGTCTCTTCAAGTGTACATGTGA 489
QY 520 GCGTGTATTAAGCCCTTGCACATATACGCGACATGAGGGCGCTTATTTGTTAAAT 579
Db 490 GGTGCGCAATTTTCACTTCCAACTGAGCAGCTCTTGAAGAAATCTGTACTGCAAGAC 549
QY 580 CACCATATTTCACTTATCAAGAGAGAGCAACTTAAGCAAGCTTGAGGGTGAACATGAA 639
Db 550 CATTTCGCTCAGC-TCTTAAGAGAGAGGAAATTACACCACTTATTAATCCGCTTCC 608
QY 640 ATGAATTCAGCAGACACAGAGAGTTACTGACAGATCATATACAGCCGACCAATGTAT 699
Db 609 ATCAACGCTTCGACGCGCAGAGATGCGCCGCTGTACAGAGAGCTTCCTGTGAA 668
QY 700 T 700
Db 669 T 669

RESULT 2
US-10-152-319A-579/C
Sequence 579, Application US/10152319A
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 579

LENGTH: 504
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. AI008930
US-10-152-319A-579

Query Match 7.6%; Score 75; DB 6; Length 504;
Best Local Similarity 58.1%; Pred. No. 1e-11;
Matches 132; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 122 AGAATGATGGCATGTGTACAGAGCTGTCTATCTGTGACAAATTAATGACATTAACA 181
Db 432 AGACCTGTGACAGCCCTGCCAAGAGAGCTGTGTACCTATGAGAGCGGCTGTGCAGACAAG 373
QY 182 GAATCTATCAAAAGCTTTGTTCAGATGATGCAATGCAAGGCACTGTCAAGCTTGCA 241
Db 372 TCATTTTCCACACACTCTTGTCTGTCTGCAAACTGCGACACCAACTGACGCTGGGCA 313
QY 242 ACTACATTCCTTTGAGGAGTCTTATCTGTAGACCACTTTGATCAGCTCTTCAAAAC 301
Db 312 GTTACGCTGCATGACAGCGTAATTTTACTGCAAACTGCACTTTCAGCAGCTGTTTAA 253
QY 302 AACTGCGAGTTTGATTAAGCTTTGAAGTACACCAAAATGTG 348
Db 252 GCAAGGCACTACGATGAGGGGTTTGTGCTAAACACACAGAGAG 206

RESULT 3
US-10-152-319A-2070
Sequence 2070, Application US/10152319A
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 2070
LENGTH: 853
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. NM_057144
US-10-152-319A-2070

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Query Match          4.5%; Score 44.4; DB 6; Length 853;
Best Local Similarity 54.2%; Pred. No. 0.0047;
Matches 90; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY      410 GTGGAACAAGAGAAATGTTTTGGCTGCACAGAAAACGTGTACCACAGAAAAAGTAT 469
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       50 GGGGTGGAGGTGCACAAATGTGTGAGCCTCGCGCAAGAGCGTGTACCATTGCAACAAATCC 109

QY      470 CAGCGAATGCGACGCCATACCATAGAAGCTGTTCACATGAGCAGCACGAGCGTGTTAA 529
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      110 AGTCAATGGGAGGAGAGCTTCCTTAAGACTGTTCACATGCGATGCCCTGCAGGAAGCTC 169

QY      530 TTAAGCCCTTCCAACATATACCGACATATGAGGGGCCCTATATATTGTA 575
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      170 TGAACAGCACCAACAGTGGAGCTCATGAGTCAAGATCTACTGTAA 215

RESULT 4
US-10-240-453--182
: Sequence 182, Application US/10240453
: GENERAL INFORMATION:
: APPLICANT: OLEK, Alexander
: APPLICANT: PIEPENBROCK, Christian
: APPLICANT: BERLIN, Kurt
: TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
: TITLE OF INVENTION: Transcription
: FILE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
: FILE REFERENCE: 5013.1009
: CURRENT APPLICATION NUMBER: US/10/240,453
: PRIOR FILING DATE: 2002-10-02
: PRIOR APPLICATION NUMBER: PCT/EP01/03973
: PRIOR FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: DE 10019058.8
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: DE 10019173.8
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: DE 10032529.7
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: DE 10043826.1
: PRIOR FILING DATE: 2000-09-01
: NUMBER OF SEQ ID NOS: 350
: SEQ ID NO 182
: LENGTH: 9515
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-453--182

Query Match          4.3%; Score 42.2; DB 6; Length 9515;
Best Local Similarity 53.3%; Pred. No. 0.04;
Matches 89; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY      806 GTTTTACTCTAATCTAGCTCAATTAATTTGAGTGTGAACATAATATTTGCTACCTTTG 865
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      6177 GTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 6236

QY      866 TGCTAGAGTTTTTGACCTTTGTTGCTGTGCTTCACATGTATATATGCAATGTGTAATG 925
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      6237 TTTCGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGTTAATTTAAATT 6296

QY      926 AGATTGATATTAACATGTTTGTGCTGTCGCCAGTGCATGCAATCTTT 972
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      6297 ATATATATATTTATATAGATTTTTTATTTATAGGAGTATTAAGTAAGATT 6343

RESULT 5
US-09-724-676--43070
: Sequence 43070, Application US/09724676
: GENERAL INFORMATION:
: APPLICANT: Comugen LTD
: TITLE OF INVENTION: Variants of alternative splicing

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; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43070
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-43070

Query Match                               4.1%; Score 40.4; DB 5; Length 294;
Best Local Similarity 61.3%; Pred.No. 0.045;
Matches 65; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

OY    410 GTGCAACAAGAGAATAATGTTTGGCTGCACAGAAAACGTCTACCCAAAGAAAAGTAT 469
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     99 GGGGGGGAGGCCAANAATGTGGAGCCTGTGAANAAGACCGTTCACCATGCAGAAATCC 158

OY    470 CAGCCAATGGCACGCCCATACCATTAAGACTGCTTCCATGCAGCCA 515
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     159 AGTGCAATGGAAGAGATTCCACAGAGCTGTTCCACTGCAGACCA 204

RESULT 6
US-09-724-676-43076
; Sequence 43076, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43076
; LENGTH: 334
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-43076

Query Match                               4.1%; Score 40.4; DB 5; Length 334;
Best Local Similarity 61.3%; Pred.No. 0.047;
Matches 65; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

OY    410 GTGCAACAAGAGAGAATAATGTTTGGCTGCACAGAAAACGTCTACCCACAGAAAAGTAT 469
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     99 GGGGGGGAGGCCAANAATGTGGAGCCTGTGAANAAGACCGTTCACCATGCAGAAATCC 158

OY    470 CAGCCAATGGCACGCCCATACCATTAAGACTGCTTCCATGCAGCCA 515
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     159 AGTGCAATGGAAGAGATTCCACAGAGCTGTTCCACTGCAGACCA 204

RESULT 7
US-09-724-676-43075
; Sequence 43075, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43075
; LENGTH: 730
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-43075

Query Match                               4.1%; Score 40.4; DB 5; Length 730;
Best Local Similarity 61.3%; Pred.No. 0.06;

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2002, 22:05:53 ; Search time 2618 Seconds

(without alignments)
10983.030 Million cell updates/sec

Title: US-09-928-412-1

Perfect score: 988
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Scoring table: IDENTIFY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
3: gb_in:*
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17: em_hum:*
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31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	988	100.0	988	6	ARI73368	ARI73368 Sequence
2	984.8	99.7	988	6	E29450	E29450 Transcripti
3	953.8	96.5	957	8	AB023479	AB023479 Nicotiana
4	737.6	74.7	898	8	AF184109	AF184109 Nicotiana
5	587	59.4	615	8	AB079513	AB079513 Nicotiana
6	378	38.3	1036	8	AB079510	AB079510 Populus k
7	353	35.7	728	8	AF187105	AF187105 Helianthu
8	332	33.6	573	6	AX412728	AX412728 Sequence
9	332	33.6	610	8	AF370569	AF370569 Arabidops
10	331	33.5	886	8	AY085377	AY085377 Arabidops
11	322.2	32.6	873	8	AY072143	AY072143 Arabidops
12	309	31.3	904	8	AF197567	AF197567 Nicotiana
13	308.4	31.2	813	8	AF197568	AF197568 Nicotiana
14	300.4	30.4	897	8	AF049917	AF049917 Petunia x
15	286.8	29.0	1015	6	ARI23331	ARI23331 Sequence
16	286.8	29.0	1015	6	E15767	E15767 Gossypium h
17	269	27.2	930	8	AF135591	AF135591 Zea mays
18	237.8	24.1	956	8	AF187103	AF187103 Helianthu
19	236.2	23.9	912	8	AF187104	AF187104 Helianthu
20	229.2	23.2	1563	8	AB079512	AB079512 Arabidops
21	193.4	19.6	631	8	AY091249	AY091249 Arabidops
22	193.4	19.6	977	8	AY063924	AY063924 Arabidops
23	193.4	19.6	991	8	AY084361	AY084361 Arabidops
24	192.4	19.5	694	8	AF370574	AF370574 Arabidops
25	180	18.2	848	8	AF443117	AF443117 Gossypium
26	179.8	18.2	882	8	AFRNAATL2	X91398 A. thaliana
27	174.8	17.7	948	8	AY094448	AY094448 Arabidops
28	173.6	17.6	603	6	AX412775	AX412775 Sequence
29	173.6	17.6	603	8	AY122901	AY122901 Arabidops
30	170	16.2	966	8	NFLIMDOM	V11002 N. tabacum m
31	157.6	16.0	960	8	AF116851	AF116851 Nicotiana
32	150.8	15.3	3229	8	AY059790	AY059790 Arabidops
33	134.4	13.6	994	8	AF047353	AF047353 Helianthu
34	121.6	12.3	1948	8	AB079511	AB079511 Populus k
35	115	11.6	130154	2	AC125482	AC125482 Medicago
36	114	11.5	1773	8	AF184885	AF184885 Nicotiana
37	110.2	11.2	1880	8	AF116849	AF116849 Helianthu
38	105.8	10.7	133658	2	CNS08CQ	AL837527 Oryza sat
39	102.2	10.3	1140	8	ATLIMI	X74319 A. thaliana
40	102.2	10.3	100746	8	AC005469	AC005469 Genomic s
41	79.8	8.1	1439	8	HASF3DNA	X64392 H. annuus SF
42	79.6	8.1	473	11	G71367	G71367 VE0059311FM
43	78.2	7.9	1081	6	AX046338	AX046338 Sequence
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ALIGNMENTS

RESULT 1
LOCUS ARI73368 988 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6303847.
ACCESSION ARI73368
VERSION ARI73368.1 GI:11912859
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 988)
AUTHORS Kawoaka, A. and Ebinuma, H.
TITLE DNA encoding a transcription factor controlling phenylpropanoid
biosynthesis pathway
JOURNAL Patent: US 6303847-A 1 16-OCT-2001;

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FEATURES
source 1. .988 /organism="unknown"
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Best Local Similarity 100.0%; Pred. No. 2e-250;
Matches 988; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
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DEFINITION
Transcriptional factor regulating phenylpropanoid biosynthesis
pathway.
ACCESSION
E29450.1 GI:13021011
VERSION
JF 1999276181-A/1.
KEYWORDS
unidentified.
SOURCE
unclassified.
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 988)
AUTHORS
Akiyoshi, K. and Hiroyasu, E.
TITLE
Transcriptional factor regulating phenylpropanoid biosynthesis
PATENT: JP 1999276181-A 1 12-OCT-1999;
JOURNAL
NIPPON PAPER IND CO LTD
OS
Nicotiana tobaccum
PN
JP 1999276181-A/1
PD
12-OCT-1999
PE
01-APR-1998 JP 1998125171
PR
AKIYOSHI KAWABOKA, HIROYASU EBINUMA
PI
C12N15/09, A01H5/00, C12N5/10, C12P21/02//C12N15/09, C12R1:91),
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(C12N5/10, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
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Db	961	ATGCAATCTTTGAGCGGCGCGGAATTC	988
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LOCUS			
DEFINITION	AB023479	957 bp	mRNA
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			PLN 24-MAY-2000
ACCESSION	AB023479		
VERSION	AB023479.1	GI:5689135	
KEYWORDS	transcription factor Ntlim1; Ntlim1.		
SOURCE	Nicotiana tabacum cell_line:SRL	CDNA	to mRNA.
ORGANISM	Nicotiana tabacum		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Asperidae; easterides I; Solanales; Solanaceae; Nicotiana.		
REFERENCE	1 (sites)		
AUTHORS	Kawaoka,A., Kaotchien,P., Yoshida,K., Endo,S., Yamada,K. and		
	Ebinauma,H.		
TITLE	Functional analysis of tobacco LIM protein Ntlim1 involved in		
	lignin biosynthesis		
JOURNAL	Plant J.	22 (4),	289-301 (2000)
MEDLINE	20307428		
REFERENCE	2 (bases 1 to 957)		
AUTHORS	Kawaoka,A. and Yoshida,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (08-FEB-1999)	Akiyoshi Kawaoka, Nippon Paper Industries,	
	Central Research Laboratory, 5-21-1 Oji, Kita-ku, Tokyo 114-0002,		
	Japan (E-mail:akiyoshi.kawaoka@nifty.ne.jp,		
	Tel:81-3-3911-5106(ex.291), Fax:81-3-3914-5350)		
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QY 915 AATGTTGAATGAGATTGAATATACATGTTTGTGCTGCCAGTGCATGCAATCTT 971
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LOCUS Nicotiana tabacum LIM domain protein WLM1 mRNA, complete cds.
DEFINITION AF184109
VERSION AF184109.1 GI:5932412
KEYWORDS
SOURCE Nicotiana tabacum.
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE
AUTHORS Eliasson, A., Hammann, P. and Steinmetz, A.
TITLE Nicotianin, a protein encoding the tobacco LIM domain
protein NtWLM1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 898)
AUTHORS Eliasson, A., Hammann, P. and Steinmetz, A.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-1999) Institute of Plant Molecular Biology, CNRS,
12 rue du General Zimmer, Strasbourg 67084, France
FEATURES
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Best Local Similarity 95.5%; Pred. No. 3.4e-184;
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QY 160 GACAAATTAACAGCAATACAGAAATCTATACAAAGCTTTGTTGATGATGATGATG 219
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QY 220 AAGGGCAGCTGCAAGCTGGCACTACAAATCTATACAAAGCTTTGTTGATGATG 279
D 121 AAGGGCAGCTGCAAGCTGGCACTACAAATCTATACAAAGCTTTGTTGATGATG 180
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LOCUS Nicotiana tabacum Ntlim1 mRNA for transcription factor LIM, complete cds.
DEFINITION AB079513
ACCESSION AB079513
VERSION AB079513.1 GI:18565123
KEYWORDS
SOURCE Nicotiana tabacum (strain: Samsun NN) cDNA to mRNA.
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE
AUTHORS Kumagai, D. and Kawai, S.
TITLE LIM of woody plant
JOURNAL Published Only in Database (2002)
REFERENCE 2 (bases 1 to 615)
AUTHORS Kumagai, D. and Kawai, S.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-2002) Shinya Kawai, Tokyo University of Agriculture and Technology, Department of applied Biological Science, 3-5-8 Saiwai-cho, Fuchu, Tokyo 183-8509, Japan
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DEFINITION Populus kitakamiensis Pklim1 mRNA for transcription factor LIM,
complete cds.
ACCESSION      AB079510
VERSION      AB079510.1 GI:18565111
KEYWORDS
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SOURCE      Populus kitakamiensis cDNA to mRNA.
ORGANISM      Populus kitakamiensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
1
REFERENCE
  1. Kumagai, D. and Kawai, S.
  LIM protein of woody plant
  Published Only in Database (2002)
  2 (bases 1 to 1036)
AUTHORS      Kumagai, D. and Kawai, S.
TITLE      Direct Submission
JOURNAL      Submitted (05-FEB-2002) Shinya Kawai, Tokyo University of
  Agriculture and Technology, Department of Applied Biological
  Science, 3-5-8 Saiwai-cho, Fuchu, Tokyo 183-8509, Japan
  (E-mail:skawai@cc.tuat.ac.jp, Tel:81-42-367-5862)
FEATURES
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Best Local Similarity 79.5%: Pred. No. 4.1e-89;
Matches 447: Conservative 0; Mismatches 115; Indels 0; Gaps 0;
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  170 TGTGAAGCCATGCGATTTTGCAGGAGACACAGAAATGATGCATGTGACAGAGCTGTG 229
QY 151 TATCTGTTGACAAATTAAGTATCAAGATTAACAGATCTATCAAAAGCTTTTGCAGATGC 210
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  230 TATCTGTTGACAAATTAAGTATCAAGATTAACAGATCTATCAAAAGCTTTTGCAGATGC 289
QY 211 CATCACTGCAAGGGCACTGTCAAGCTTGGCACTTACATTTCTTTGAGGAGTTCTATAC 270
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  290 CATCACTGCAAGGGCAAGCCCTCAAGCTTGGCACTTACATTTCTTTGAGGAGTTCTCTAC 349
QY 271 TGTAGACCACTTTGATCAGCTCTTCAACAACACTGGCAGTTTGGATTAAGCTTTGAA 330
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  350 TGTAGACCACTTTTATATCACTGTTCAAAAGACTGGAGCTTTGACAAAAGCTTTGAG 409
QY 331 GGTACACAAAAAATGTGAAGCCACAGAAACCATTTGACAGTGAAGAACACAGAGTAGCC 390
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  410 GGTACACAAAAAATGTGAAGCCACAGAAACCATTTGAGTGAAGAACAGTGTGACACT 469
QY 410 GGTACACAAAAAATGTGAAGCCACAGAAACCATTTGAGTGAAGAACAGTGTGACACT 469
QY 391 AAGTGAACAAGCATTTTGTGTGAACAAGAGAAATGTTTGGCTGCAAGAAACTGTG 450
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  470 AAGTGTGACCAAGTGTGCGCCGAGACAGAAAGATGTTTGGCTGCAAGAAACTGTG 529
QY 451 TACCCACAGAAAAGTATCAGCCATGACGCGCATTAACAGTGAAGAGCTTCCATGCG 510
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  530 TATCCACTGAGAGAGTTTGTGGAATGGAAGTCTTACACAGAAAGCTTTCAATGCG 589
QY 511 AGCCACGAGAGCTGTGTAATTAAGCCCTTCCAACTATACGACAGATGAGGGGCGCTTATAT 570
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  590 ATCCACGAGAGAGTATCAATTAAGCCCATCAACTATGACATGAGAGTGAAGGCTCTAC 649
QY 571 TGTAAACATTCACCATTTATCACTTACAGGAGAGAGGCAAGTATGAGGCT 630
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Db	710	GATATTGAGAGGACTCATGA 731	
RESULT 7			
LOCUS	AF187105		
DEFINITION	Helianthus annuus LIM domain protein WLIM1 (WLIM1) mRNA, complete cds.		
ACCESSION	AF187105		
VERSION	AF187105.1	GI:5932435	
KEYWORDS			
SOURCE	Helianthus annuus.		
ORGANISM	Helianthus annuus		
REFERENCE	1	(bases 1 to 728)	
AUTHORS	Mundel,C., Baltz,R., Eliasson,A., Bronner,R., Gass,N., Krauter,R.,		
TITLE	Everard,J.L. and Steimetz,A.		
JOURNAL	A LIM domain protein from sunflower localizes to the cytoplasm		
REFERENCE	and/or the nucleus in a wide variety of tissues and associates with		
AUTHORS	the phragmoplast in dividing cells		
TITLE	Plant Mol. Biol. (1999) In press		
JOURNAL	2 (bases 1 to 728)		
REFERENCE	Eliasson,A., Gass,N., Hamann,P. and Steimetz,A.		
AUTHORS	Direct Submission		
TITLE	Submitted (17-SEP-1999) Institute of Plant Molecular Biology, CNRS,		
JOURNAL	12 rue du General Zimmer, Strasbourg 67084, France		
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Query Match	35.7%	Score 353;	DB 8; Length 728;
Best Local Similarity	78.6%	Pred. No. 1.8e-82;	
Matches 422; Conservative	0;	Mismatches 115;	Indels 0; Gaps 0;
Qy	100	ATGGCTTTTGAGGAGACACAGAAATGCAATGGCAGTGCACAGACCTGTATCTGGTT	159
Db	1	ATGGGATTGAGGAGGACACACAGAAATGCAATGGCAGTGCACAGACCTGTATCTGGTT	60
Qy	160	GACAAATTAACATGAGATACAGATCATATACACAAGCTTTTCAGATGCATCAGGC	219
Db	61	GACAAATTAACATGAGATACAGATCATATACACAAGCTTTTCAGATGCATCAGGC	120
Qy	220	AAGGCACTGTCAAGCTTGGCACTACAAATTCCTTTGAGGAGATTCATACATGAGACA	279
Db	121	AATGGCACACTAAAGGCTCAGTACAAACCTTTGAGGAGATTCATACATGAGACA	180
Qy	280	CACCTTGATCAGCTCTTCAACAACAAAGCGGCTTTGGATTAACCTTTGAAAGTACACA	339
Db	181	CACCTTGATCAGCTCTTCAACAACAAAGCGGCTTTGGATTAACCTTTGAAAGTACACA	240

QY	340	AAAAATGTAACGCACAGAAACCATTGACAGTGAAGAAACACAGGTAGCCAAAGTGACA	399
Db	241	AACTTTTGTGAACCAACCGAATGATGGCGAGAAACCAATAGCAATTAAGTCTCG	300
QY	400	ACCATGTTTGTGGGAACAGAGAGAAGAAATGTTTGGCTGCAAGAAAACTGTACCCAAACA	459
Db	301	ACTATGTTTGTGGGAACAGAAATAGTGTGGGTGTGAACACAGATTACCCAAAC	360
QY	460	GAAAGATATACAGCCAAATGACAGCCCATATACATTAAGAGCTGCTCCATATGACGACGGA	519
Db	361	GAAAGAGTTTCTGTGAACGGAATGCATACCAACAAAGTTGCTTTAAATGTAGCATGGA	420
QY	520	GGCTGTGTAATTAAGCCCTTCGAATATACCGACATAGAGGGCGCTTATATGTAAACT	579
Db	421	GGTTGTACATTAAGCCCATCGAATTAATATATGCGCATGAAGGTCAATCTCTACGACAGAC	480
QY	580	CACCAATATTCACACTTATACAGAGAAAGGCGCACTTAAGCAACCTTGAGGGTGACCAT	636
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DEFINITION	Sequence 492 from Patent WO0222675.	Linear	PAT 14-JUN-2002
ACCESSION	AX412728		
VERSION	AX412728.1	GI:21445186	
KEYWORDS			
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
AUTHORS	1 Glazebrook, J., Wang, X., Dangl, J. L., Eulgem, T. and Zhu, T.		
TITLE	Plant genes, the expression of which are altered by pathogen infection		
JOURNAL	Patent: WO 022675-A 492 21-MAR-2002; Syngenta Participations AG (CH) ; UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL, (US) ; Glazebrook, Jan (US) ; Wang, Xun (US) ; Dangl, Jeffrey L. (US) ; Eulgem, Thomas (US)		
FEATURES	location/qualifiers		
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Best Local Similarity	76.5%;	Pred. No. 6.4e-77;	Length 573;
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		Indels	0;
		Gaps	0;
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QY	220	AAGGCACTGTCAAGCTTGGCACTACTAATTCCTTTGAGGAGATTCTATCTGATGACCA	279
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QY	280	CACTTTGATCAGCTCTCAACAAACCTGGCAGTTTGGTAAAGCTTTGAAGTACACCA	339
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Db	361	GAAAGAGTTTCTGTGAACGGAATGCATACCAACAAAGTTGCTTTAAATGTAGCATGGA	420
QY	520	GGCTGTGTAATTAAGCCCTTCGAATATACCGACATAGAGGGCGCTTATATGTAAACT	579
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QY	580	CACCAATATTCACACTTATACAGAGAAAGGCGCACTTAAGCAACCTTGAGGGTGACCAT	636
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Matches 413; Conservative 0; Mismatches 133; Indels 1; Gaps 1;

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625 GAGGGTG 631
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RESULT 12
AF197567 904 bp mRNA linear PLN 13-NOV-2000
LOCUS Nicotiana tabacum pollen specific LIM domain protein 1a mRNA,
DEFINITION complete cds.
ACCESSION AF197567
VERSION AF197567.1 GI:6467902
KEYWORDS
SOURCE Nicotiana tabacum.
ORGANISM Nicotiana tabacum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE Sweetman,J., Spurr,J., Eliasson,A., Gass,N., Steinmetz,A. and
Twell,D.
```

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TITLE Isolation and characterization of two pollen-specific LIM domain
JOURNAL protein cDNAs from Nicotiana tabacum
REFERENCE Sex. Plant Reprod. 12, 339-345 (2000)
AUTHORS 2 (bases 1 to 904)
TITLE Sweetman,J. and Twell,D.
JOURNAL Direct Submission
Submitted (21-OCT-1999) Biology, University of Leicester,
University Road, Leicester, Leics LE1 7RH, UK
FEATURES
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BASE COUNT 277 a 174 c 186 g 267 t
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Matches 396; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

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116 ATGACGTTTCAGAGAAACAGCAAAAGTCAGTCTTGAGAAAGCGTATCTGTG 175
160 GACAAATTAAGTGCAGATTAACAGATCTATCAACAAGCTTTGTCAGATCCACTGC 219
176 GATCGTCTTCTCGTGAATTCGATTAACAGAGCTTTGATGAGTCTACCACTGC 235
220 AAGGGCACTGTCAAGCTTGGCACTACATCTCTTGAAGGAGTGTATCTGTAGACA 279
236 AAAAGTACTCTCAAGCTCACTAATTTCACTCTTGAAGGGGTAATTTACTGTAGCCCT 295
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340 AAAAATGTAAGCCAGAAACCCATTTGACAGTGAAGAACACACAGTACGCAAAAGTACA 399
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400 AGCATGTTTGGTGGACAAAGAGAAATGTTTGGCTGCGCAAGAAACTGTCTACCCACA 459
416 AGTTATTTCAGAGCAGAGGAAATGTGTGGCTGCACTAAACTGTGTATCCGATT 475
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520 GGCTGTGTAATTAAGCCCTTCCAACTATACCGACATAGAGGGGCGCTTAATTTGTAACAT 579
536 GGCTGTACATAAAGCCCATCAAAATTAATTTGACATGAAGAGGCTTTATTTCAAGCAC 595
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DB 514	AGTCATGAGAGGCGTGTCAATTAAGCCCATCAATTTACATTTGACATGAGGGAAGGCTTAT	573	0	146	DB 8	897	71.6%
QY 571	TGTAAACATCACCATTATTTCACTTATCAAGAGAAAGGCACTTAAGCAAGTTAGGCT	630	0	146	DB 8	897	71.6%
DB 574	TGCACACACACCATATATCACTTTCAAGAGAAAGCAATTAACAGCAGCTAGTCT	633	0	146	DB 8	897	71.6%
QY 631	GACCATGAAA 640		0	146	DB 8	897	71.6%
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RESULT 14							
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DEFINITION	Petunia x hybrida PGPS/D1 (PGPS/D1) mRNA, complete cds.						
ACCESSION	AF049917						
VERSION	AF049917.1						
KEYWORDS	GI:4105771						
SOURCE	Petunia x hybrida.						
ORGANISM	Petunia x hybrida.						
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Petunia.						
AUTHORS	1 (bases 1 to 897)						
TITLE	Guyon, V.N., Astwood, J.D., Garner, E.C., Dunker, A.K. and Taylor, L.P.						
JOURNAL	Isolation and characterization of cDNAs expressed in the early stages of flavonol-induced pollen germination in petunia						
MEDLINE	Plant Physiol. 123 (2), 699-710 (2000)						
PUBMED	20317212						
REFERENCE	10859200						
AUTHORS	2 (bases 1 to 897)						
TITLE	Guyon, V., Astwood, J.D. and Taylor, L.P.						
JOURNAL	Direct Submission						
FEATURES	Submitted (23-FEB-1998) Genetics and Cell Biology, Washington State University, Science Hall, Pullman, WA 99164-4234, USA						
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Db 151 GATATCAAGATGACATGCTGGAGAACATCAAAAGTGACGTCTTGATATAAACTGT 210
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 Db 211 GATATGGTGTGATCGCTGCTGTGATTAACCGTGTCTATCACAAGGCTTTGTTCAAGATG 270
 QY 210 CCATCTACGTCAAGGGGACGTGTCAAGCTTGCAACTACATTCCTTTGAGGAGATCTTATA 269
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RESULT 15
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 LOCUS ARI23331 1015 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 1 from patent US 6169174.
 ACCESSION ARI23331
 VERSION ARI23331.1 GI:14108297
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1015)
 AUTHORS Hasegawa,O., Aotsuka,S., Takenishi,S. and Uchimiya,H.
 TITLE Cotton plant gene
 JOURNAL Patent: US 6169174-A 1 02-JAN-2001;
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Query Match 29.0%; Score 286.8; DB 6; Length 1015;
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 Matches 394; Conservative 0; Mismatches 152; Indels 6; Gaps 1;

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 Db 433 CTCTGTTTGGTGCACAGAGAAAATGTGGGCTTTCTAAGACTGCTTATCCAAATTGA 492
 QY 462 AAAGTATCAGCCAAATGCGACGCGCATATAGAGCTGCTTCCAAATGCAAGCCAGAG 521
 Db 493 GAGGTTTACTGTGAATGGGACATATACCAAGAGAGCTGCTTCAAGTGAATGATGAGG 552
 QY 522 CTGTGATTAATAGCCCTTCCAACTATACCGCACATGAGGGGCGCTTATATTGTAACATCA 581
 Db 553 GTCTACCATTAAGCCCATCAAACTATATAGCACATGAAGGTAAACTCTACTGCAAAACATCA 612
 QY 582 CCATATTCAACTTATCAAGGAGAAAGGCAACTTAAGCAAGCTTGAAGGTTGACCATGAAT 641
 Db 613 CCATATCCAACTCTTCAAGSAGAAAGAACTACAGCCAACTGAGACCGAACGAGAGAA 672
 QY 642 GAATTCACGAC 653
 Db 673 ACNAGCGCGCAC 684

Search completed: November 22, 2002, 23:02:20
 Job time : 2622 secs

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DR WP1: 2000-579369/54.

XX New isolated polynucleotide encoding a plant transcription factor for
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
PT having modified gene expression or modified activity of a polypeptide
XX -

PS Claim 1: Page 48; 747pp: English.

XX The present invention relates to novel plant transcription factors from
CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding
CC sequence for one such transcription factor. The transcription factor may
CC be used to produce a plant having modified gene expression such as a
CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
CC mahogany species or to modify the activity of a polypeptide in a plant.
CC The transcription factors of the present invention are members of the
CC following families of regulatory proteins: bZIP, bZIP family of G-box
CC binding factors, basic helix-loop-helix zipper,
CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2
CC and ERBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements
CC and MYB.

SO Sequence 983 BP; 273 A; 237 C; 239 G; 234 T; 0 other:

Query Match 34.0%; Score 336.4; DB 21; Length 983;
Best Local Similarity 75.5%; Pred. No. 3.2e-86;

Matches 418; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

OY 100 ATGGCTTTTGCAGGAAACACAGAAATTCATCGCATGGCATAAGACTGTATCTGTT 159
DB 103 ATGGCATTCGCGAGNACCACCCAGNAGTGCACTGGCTGGAGAACAAGCTATCTGGTG 162
OY 160 GACAAATTAACTGCAGATTAACGAATCTATCAACAAGCTTGTTCAGATGCCATCACTGC 219
DB 163 GACAGCTCACAGCTGACAAATAGAAATCAACACAAAGGCTGCTTCAGATGCCACATTGC 222
OY 220 AAGGCACTGTCAAGCTTGGCAACTCAATTCTTTGAGGAGTTCTATCTGTAGACCA 279
DB 223 AAAGGACTCTTCMACTTGGGAACTATTAATTCATTTGAAGGAGTCTTGTACTGCGGCG 282
OY 280 CACTTGTATCAGCTCTTCAAACCAACCTGGCAGTTGGATAAAGCTTGAAGGTACACCA 339
DB 283 CATTTTCATCAGCTCTTCAAGAGAACTGCGACCTCGAANAAGCTTGAAGGAACCCCC 342
OY 340 AAAAATGTGAAGCCACAGAAAACCTTGTACAGTGAAGAACACAGGTAGCCAAAGTGACA 399
DB 343 AAGATTGCAAAAGCCAGAAAACCCCTGCATGAGAGAGAACCTCGCAGGACCAACACCTCC 402
OY 400 AGCATGTTTGGTGCAGCAAGAGAAATGTTTTGGCTGCAGAAAACTGTCTACCCAACA 459
DB 403 AGTATGTTGGGGGAGCCGAGACAAATGTAGAGCTTAGAAGACACCGCTTACCCGAC 462
OY 460 GAAAGGATATGAGCAATGAGCAGCGCATACATTAAGACTGCTTCATGAGCCAGCGGA 519
DB 463 GAANAAGTGACGTTTAATGGAGCTCATACCAACAAGACTCTTCAAAATGCAACCCAGCGG 522
OY 520 GGCTGTGTAATTAAGCCCTTCCAACTATACCCACATATGAGGGGCGCTTATATTGTAACAT 579
DB 523 GGGTGGCGATCAGCGCATTCACACTAGCTGGCGGACGAGGGGAAACTCTACTCGACGAC 582
OY 580 CACCATATTCAACTTATTCAGGAGAGAGGCAACTTAAGCAAGCTTGAGGGTGAACATGAA 639
DB 583 CACCACTACTGATCATTAAGAGAGAGGCAANTCTCAACCAACTGAGAGGGGATCATAGAG 642
OY 640 ATGAATTCACAGAC 653
DB 643 AGGGAACAATAGGC 656

RESULT 2
AAC49742
ID AAC49742 standard; DNA; 956 BP.
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AC	AAC49742;	
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DT	18-OCT-2000	(first entry)
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DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 62273.	
XX		
KM	Hybridisation assay; genetic mapping; gene expression control	
KW	protein identification; signal transduction pathway;	
KX	metabolic pathway; promoter; termination sequence; ss.	
XX		
OS	Arabidopsis thaliana.	
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
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PF	25-FEB-2000; 2000EP-0301439.	
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PR	25-FEB-1999;	99US-0121825.
PR	05-MAR-1999;	99US-0123180.
PR	09-MAR-1999;	99US-0123548.
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PR	29-MAR-1999;	99US-0126785.
PR	01-APR-1999;	99US-0127462.
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PR 26-OCT-1999; 99US-0161920.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 33.8%; Score 334.2; DB 21; Length 956;
Best Local Similarity 75.7%; Pred. No. 1,3e-85;
Matches 414; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 85 TGCCTGCTATATAGCCATGCGTTTTCAGAGAAACCAAGAAATCCATGCGATGAGAAAG 144
DB 100 TGATCTCTTACAGAAATGGCGTTTCAGAGAAACCAAGAAATCCATGCGATGAGAAAG 159
QY 145 ACTGCTATCTGTTGTTGCAATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 204
DB 160 ACAGTTTATCTTGTGCAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 219
QY 205 AGATGCCATCAGCTGCAAGGCGACTGTCAAGCTTGGCACTAATTCCTTTGAGGAGTT 264
DB 220 CGATGTCACCATTAAGCAAGGAGCTCAAGCTTGAATTAACAATCTTTGAAGGAGTT 279
QY 265 CTATACGTGATAGCAACCTTGTGATCAGCTCTTCAAAACAACTGGACATTTGATTAAGC 324
DB 280 CTCTACTGACAGCACCAATTTTCGATTCAAACTTCAGAGAACTGAACTTGAAGAAAGC 339

Qy	325	TTTGAAGGTACACCAAAAAATGTGAGGCCACACGAAGAACCCATTGACAGTAGAANACACAG	384
Db	340	TTTGAAGGACACCAAAAGTTGGGAAACCTGATGAGCCTTTGGAGGAGAGACCTGCT	399
Qy	385	GTAGCAAAAGGACAGCATTTGGTGGGAACAGACAGAAATGTTTGGCTGCAACAAA	444
Db	400	GGAAACCAAGTTTCCAATATTTTGGTGGAAACAGAAAGAAATCCGTGGTGTGGACAAA	459
Qy	445	ACTGTCFACCCCAACGAAAGAGGTATCAGCCAGGACAGCCATTCATTAAGAGCTGCTC	504
Db	460	ACCGTGTTATCCAAATTTGACAAAGCTTTCGGTGAATGGAACATTTGATCCCAAGAGCTGCTTC	519
Qy	505	CAATGCACGCCACGGAGGCTGTGTATTAAGCCCTTCCAACTATACCCACATGAGAGGGCGC	564
Db	520	AAGTGTACAACTGGAGGGGTGACACATAAGCCCTTCGAATTACATAGCTCAGAGGGTAAG	579
Qy	565	TTTATATTGTTAAACATCACCATATTTCAACTTATCAAGAGGAAGGGCACTTTAAGCAAGCTT	624
Db	580	CTATATTGCACGATCATCATATTTCAAGTATCAAGAGGAAGAAACTTTGAGCCAGCTC	639
Qy	625	GAGGCTG 631	
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PR	05-AUG-1999	9905-0147935
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
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PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162143.

Query Match	33.6%	Score 332;	DB 21;	Length 969;
Best Local Similarity	76.5%;	Pred. No. 5.8e-85;		
Matches 407; Conservative	0;	Mismatches 125;	Indels 0;	Gaps 0;

QY 100 ATGGCTTTTGCAGGACACACAGAATGCATGGCATGTGACACAGACTGTCTATCTGTT 159

Db 127 ATGGCTTTCGACGACACCCAGAATGCATGGCCTGTGACAAACAGTTTATCTTGTCT 186

160 GACCAATTAACTGCAGATAACAGAATCTATCACAAAGCTTGTTCAGATGCCATCACTGC 219

Db 187 GACAGTTAACCGCCGATAACCGGGTCTACCACAAAGCTTGTTCGGATGTCACCAATTGC 246

220 AAGGCACTGTCAAGCTTGGCACTACAATTCCTTGAGGGAGTTCATACTGTAGACCA 279

Db 247 AAAGGAAGCTCTCAAGCTTAGCAATTACAAGCTCTTGAAGGAGTTCTCTACTGCAGACCA 306

QY 280 CACTTTGATCAGCTCTTCAACAACAACCTGGCAGTTTGGATAAAAGCTTTGAAGGTACACCA 339

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340 AAAAATGTGAAGCCACAGAAACCCATTGACAGTGAAGAACCACAGGTAGCCAAAGTGACA 399

DB 36 / AAGAT1GGGAACCTGATAGGCCCT11GGAGGGAGAGGACCTGCTGGAACTAAAG111CG 420

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[illegible][illegible]

607
658

RESULT 4
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1/-OCT-2000 (first entry)
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DE ALABAMA DNA LABORATORY ID NO: 5537.
XX

KW protein identification; signal transduction pathway;

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06-SEP-2000
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QY 66 TTTTGTCTGTAACCTGCTGTATATAGCCATGCTTTGGCAGAACACACAGAA 125
DB 26 TGTCTGTTGAAGAGAGACGCGCGGCGCATGCGCACCTCTCCAGGGGAGACACCAA 85
QY 126 ATGCATGCGATGACAAAGCTGTCTATCTGTTGACAAATTAATCAATATACAGAA 185
DB 86 GTTCACCGCGCTGCACAAAGCGGTGACCTTTGGGACAACTCAACCCGACCAACCCCAT 145
QY 186 CTATCAACAAGCTTTGTTAGATCCATCACTGCAAGGACACTGTCAAGCTTGGCACTA 245
DB 146 CTACACAAAGCGCTGCTCCGCTGCCACCACTGCAAGGCAACCTCAAGCTCCGCACTA 205
QY 246 CAATTCCTTTGAGGAGCTTATATCTGTAGACACACACTTTGATCAGCTCTTCAAAAC 305
DB 206 CAATCTCTTTGAGGAGTGTCTATCTGACAGCGCTCACTTGACAGAGCTTTCAAGAGAC 265
QY 306 TGGCATTTGATTAAGCTTTGAGGTACACCAAAAATGTGAAGCAGACAGAACCCAT 365

DB 266 AGGAGCTTGGACAGAGCTTCGAAAGAACTCCGAAGTTGTCAAGCCAGAAAGAACGT 325
QY 366 TGACAGTGAGAAACACAGAGTACCAAGTAGACAGCATGTTGGTGGACAGAGAGA 425
DB 326 TGGGATAGAG-----ATGCTACTAAAGTCTCAAGCCCTTTTGTGGCACCAGAGAGA 379
QY 426 ATGTTTGGCTGCAAGAAACTGTCTTACCCAAACAGAAAAAGGTATCAGCCAAATGGCACC 485
DB 380 ATGTGTGATGACAGACAGACAGTCTATCCAACTGAGAGGGTCACTGTTAATACACTAT 439
QY 486 ATACCATTAAGGCTGCTTCCAAATGAGCAGGAGGCTGTATTAATACCCCTTCCAACTA 545
DB 440 GTACCAAGAGCTGCTTCAAGTGTCTGATGAGAGGTGACACCATCAGCCCTTCACTA 499
QY 546 TACCGACATGAGGGGCGCTTATATTGTAACATCACCATTATTCACATTAACAGAGAA 605
DB 500 CATTGGCAGCAGGGGAGAGCTGTACTGACACACACACATCCAGCTGATCAAGAGAA 559
QY 606 GGGCACTTAAGCAAGCTTGAAGGTGACCATGAATGAATTC 647
DB 560 GGGGAACCTTCAGCCAGCTTGAGAAATGACACGAGAAACATTC 601

RESULT 8
AAC51693 standard; DNA: 1079 BP.
AAC51693:

DT 18-OCT-2000 (first entry)
XX
DE Zea mays DNA fragment SEQ ID NO: 69444.

KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.

XX Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139465.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.

PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0156559.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.

PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161921.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 28.8%; Score 284.2; DB 21; Length 1079;
Best Local Similarity 70.7%; Pred. No. 3.2e-71;
Matches 395; Conservative 0; Mismatches 158; Indels 6; Gaps 1;

QY 89 CGTATATAGCCATGGCTTTTCCAGAACACAGAAATGCGATGTACAGACTG 148
D 293 CGGCGATGGGCGCTCTCCAGGAGAGACCACCAAGTGCACCGCTGCCACAAGACTG 352
QY 149 TCTATCTGCTTGAATAATTAATGAGATACAGAAATGATACAAAGCTTTGATCAT 208
D 353 TGTACCTTTGTGACAGAGCTTACCGCCGACACCCATCTACCAAGAGCTGTCTCGCT 412
QY 209 GCCATCACTGCAAGGCGACCTGTCAAGCTTGGCACTACATTAATCTTTGAGGAGTTCTAT 268
D 413 GCCACCACTGCAAGGCGACCTGTCAAGCTTGGCACTACATTAATCTTTGAGGAGTTCTAT 268
QY 269 ACTGTAGACCACTTTGATGACTCTTCAAAACAACTGCGAGTTGGATAAAGCTTTG 328
D 473 ACTGACAGGCTTCACTTGCACAGCTGTTCAGAGAGGAGGAGCTTGGACAAAGCTTGC 532
QY 329 AAGGTACACCAAAATAATGTAAGGACAGAAACCATTGACAGTGAAGAAACAGAGTAG 388
D 533 AAGGAACCTCCCAAGCTTGTCAAGGACAGAAACGTTGGATGAGAAATGCTTA----- 586
QY 389 CCAAGTGAACAGCATGTTGGTGAACAGAGAGAAATGTTTGGCTCAAGAAACTG 448
D 587 CTAAAGTCTCAAGGCGCTTGTGCTGACACAGAGAAATGTTGATGAGTCAAGAACAG 646
QY 449 TCTTCCCAAGCAAAAGATATACAGCAATGACAGCCATACCATTAAGAGCTTCCAT 508
D 647 TCTATCCAACTGAGAGGCTCTTAAACAACATATGATACCAAGAGCTGCTCAAGT 706
QY 509 GCACGCAAGGAGCTGTATATAGCCCTTCCAACTATACGCGACATGAGGGGGCTTAT 568
D 707 GCTCCATGAGAGGCTGACCATGAGCCCTTCTACTACATTTGCGCAGAGGGAAGCTGT 766
QY 569 ATTGTAAACATCAACATATTTCACTTATCAAGAGAAAGGCACTTAAGCAAGCTTGA 628
D 767 ACTGCAAGGACCAACCATCCAGCTGATCAAGAGAGGGAAGCACTTCAAGCAGCTTGA 826
QY 629 GTGACCATGAATGATTC 647
D 827 ATGACCAAGAGACATC 845

RESULT 9
AAC56321
ID AAC56321 standard; DNA: 1116 BP.
XX
XX AAC56321:
DT 25-JAN-2001 (first entry)
XX
DE Pinus radiata transcription factor DNA sequence #121.
XX
KW Plant: transcription factor; gene expression: eucalyptus; pine: acacia;
KW Poplar: sweetgum; teak: mahogany; bZIP; G-box binding factor;
KW basic helix-loop-helix zipper; homeotic: homeodomain; homeobox:
KW homeodomain zipper; LIM domain; AP2; EREBS; zinc finger domain;
KW type 2 Cys2His2; CCAAT box element; MYB; ss.
XX
OS Pinus radiata.
XX
PN MO200053724-A2.
XX
PD 14-SEP-2000.

XX 09-MAR-2000; 2000MO-US06112.
PF
XX
PR 11-MAR-1999; 99US-026513.
PR 18-AUG-1999; 99US-0149485.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
PI Wood M, McGrath A, Shenk M, Glenn M;
XX WPI: 2000-579369/54.
XX
DR
XX
PT New isolated polynucleotide encoding a plant transcription factor for
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
PT having modified gene expression or modified activity of a polypeptide
PT
XX
PS Claim 1; Pages 162-163; 747pp; English.
XX
CC The present invention relates to novel plant transcription factors from
CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding
CC sequence for one such transcription factor. The transcription factor may
CC be used to produce a plant having modified gene expression such as a
CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
CC mahogany species or to modify the activity of a polypeptide in a plant.
CC The transcription factors of the present invention are members from the
CC following families of regulatory proteins: bZIP, bZIP family of G-box
CC binding factors, basic helix-loop-helix zipper,
CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2
CC and EREBS, zinc finger domains of type 2 Cys2His2, CCAAT box elements
CC and MYB.
XX
SQ Sequence 1116 BP; 311 A; 202 C; 264 G; 339 T; 0 other;
QY
Query Match 25.3%; Score 249.8; DB 21; Length 1116;
Best Local Similarity 67.2%; Pred. No. 2.4e-61;
Matches 353; Conservative 0; Mismatches 172; Indels 0; Gaps 0;
QY 100 ATGCTTTTGGAGGACCAACAGAAATGATGAGTGAAGCTTATCGTT 159
D 202 ATGCGCTTCCGCGCACACCAAGCTGCAAGCAATGTAAGAGCGTCTATTGTT 261
QY 160 GACAATTAATCTGAGATTAACAGATCTATCAAACTGTTTCAGATGCGATCTG 219
D 262 GATCAATTTGACAGCTGATTAATCTGTTTTCACAAATCTGTTCCGCTGCACTG 321
QY 220 AAGGCACTGTCAAGCTTGGCACTACATTTCTTTGAGGAGTTCTATAGTACCA 279
D 322 AATGGAACCTTAAAGCTTACCACTATTCGTTTGAAGGAGTCTTATATTCGAAACT 381
QY 280 CACTTGTATCAGCTCTCAAAACAGTGGCACTTGTATTAAGCTTGAAGTACACCA 339
D 382 CATTTTACCAAGCTGTTTAAAGAGAGAGATTTGATTAAGTTTGAAGCCATTCCT 441
QY 340 AAAAATGTGAAGCCACAGAAACCATGAGATGAGAAACACAGTAGGCAAGTACCA 399
D 442 AGAGCATCAAGAAATGACAGATGATGAGATGAGAAACACCATAGTAGGATCA 501
QY 400 AGCATGTTTGTGAGACAGAGAGAAATGTTTGGCTGCAAGAAACTGTCTACCA 459
D 502 GCATTTGTTTCCGCTACACAGGATTAATGTGTGCAATGTGGAAGACAGTACCCCAT 561
QY 460 GAAAGGTATCAGGCAATGACAGCCCATACCATTAAGAGCTTCCAAATGACAGCA 519
D 562 GAGAAAGTGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 621
QY 520 GCGTGTGTAATTAAGCCCTTCAACTATATACGCAATGAGGCGCTTATATTAACAT 579
D 622 GGTGTGTCATGAGCCCTCAAAATTAATGTTGCTCATGAGGAGCTATATTTAGGCA 681
QY 580 CACCATATTCATTAATCAAGAGAGAGGCACTTAAGCAAGCTT 624

PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151303.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159283.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 23-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161820.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 22.7%; Score 224.6; DB 21; Length 672;
Best Local Similarity 64.7%; Pred. No. 3.3e-54;
Matches 408; Conservative 0; Mismatches 124; Indels 99; Gaps 1;

QY 100 ATGGCTTTTCAGAACACAGAAATGATGGCATGACAAAGACTGTCTATCTGCTT 159
DB 1 ATGGCTTTTCAGAACACACAGAAATGATGGCATGACAAAGACTGTCTATCTGCTT 60
QY 160 GACAAATTAATCTCAGATACAGAAATCTATCACAAGCTTGTTCAGATCCATCACTGC 219
DB 61 GACAAATTAATCTCAGATACAGAAATCTATCACAAGCTTGTTCAGATCCATCACTGC 120
QY 220 AAGGCACTCTCAAGCTTGGCAACTCAATTCCTTTGAGGAGTCTTATACCTGACCA 279

DB 121 AAGGAACCTCAAGCTTAGCAATTAACAATCTTTGAGAGAGTCTCTACTGACAGACA 180
QY 280 CACCTTGATGACGCTCTTCAAAACAACTGCGAGTGGTAAAGCTTGAAGT----- 333
DB 181 CATTTGCATCAAACTTCAAGAGAACTGGAAGCTTTGAGAAAAGCTTGGAATTA 240
QY 334 ----- 333
DB 241 CCAAAAACAGATCAAAATGTGAAAAGCTTTGAGTGGGAGTTCAATTTGAATTATC 300
QY 334 -----ACACCAAAAATGTGAAGCCACAGAAA 360
DB 301 TATCTAAAGTTGATTCATATATATATGACAGGACACCAAGATTTGGCAACATGAG 360
QY 361 CCCATTGACAGTGAAGAACACAGGTAGCCAAAGTGACAGCAATGTTGGTGAACAGA 420
DB 361 CTTTGGAGGAGAGAGACCTGCTGGAACCAAACTTTGCAATATGTTGGTGAACAGA 420
QY 421 GAGAAATGTTTTGGCTGCAAGAAAAGTCTTACCCACAGAAAAGTATACGCCAATGCG 480
DB 421 GAGAAATGCGTTGGTGGACAAAACCGTATTCCAATTTGAAAGGTATGGTGAATGA 480
QY 481 ACGCATACCATTAAGAGCTGCTTCAATGACGCCAGGAGGCTGTGTAATAGCCCTTCC 540
DB 481 ACATTTGACCAAGAGAGCTGCTTCAAGTGTACATGAGAGCTGACAGATTAAGCCCTTCC 540
QY 541 AACTATACCGCATGAGGCGGCTTATATGTAATCATACCATTTCAACTATACAG 600
DB 541 AATTACATAGCTCAGAGGAGTAACTATATTTCAAGCATCATATTTCAAGTATCAAG 600
QY 601 GAGAAAGCAACTTAAGCAAGCTTGAAGG 631
DB 601 GAGAAAGCAACTTAAGCAAGCTTGAAGG 631

RESULT 11
AAA31931 standard; DNA; 396 BP.
ID AAA31931:
AC AAA31931:
AT 05-JUL-2000 (first entry)
DE Plant microsatellite marker #892.
XX
KW Plant microsatellite sequence; core repeat sequence; detection; probe;
KW DNA polymorphism; genome mapping; physical mapping; fingerprinting;
KW variety identification; genetic variability evaluation; primer; ss.
XX
OS Eucalyptus grandis.
XX
PN WO9967421-A1.
XX
PD 29-DEC-1999.
XX
PF 25-JUN-1999; 99WO-NZ00092.
XX
PR 25-JUN-1998; 98US-0105307.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Havukkala IU, Bloksberg LN, Glenn M;
XX
DR WPI; 2000-116958/10.
XX
PT New plant microsatellite markers and associated flanking species for
PT the detection of polymorphic genetic markers -
XX
PS Claim 1; Page 339; 392pp; English.
XX
CC Sequences AAA31040-A32093 represent novel plant microsatellite sequences

PR 19-JUL-1999: 99US-0144333.
PR 19-JUL-1999: 99US-0144334.
PR 19-JUL-1999: 99US-0144335.
PR 20-JUL-1999: 99US-0144332.
PR 20-JUL-1999: 99US-0144332.
PR 20-JUL-1999: 99US-0144884.
PR 21-JUL-1999: 99US-0144814.
PR 21-JUL-1999: 99US-0145086.
PR 21-JUL-1999: 99US-0145088.
PR 22-JUL-1999: 99US-0145087.
PR 22-JUL-1999: 99US-0145089.
PR 22-JUL-1999: 99US-0145192.
PR 23-JUL-1999: 99US-0145145.
PR 23-JUL-1999: 99US-0145218.
PR 23-JUL-1999: 99US-0145224.
PR 26-JUL-1999: 99US-0145276.
PR 27-JUL-1999: 99US-0145913.
PR 27-JUL-1999: 99US-0145918.
PR 27-JUL-1999: 99US-0145919.
PR 28-JUL-1999: 99US-0145951.
PR 02-AUG-1999: 99US-0146386.
PR 02-AUG-1999: 99US-0146388.
PR 03-AUG-1999: 99US-0146389.
PR 04-AUG-1999: 99US-0147038.
PR 04-AUG-1999: 99US-0147204.
PR 04-AUG-1999: 99US-0147302.
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Query Match 19.6%; Score 193.4; DB 21: Length 991;

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DT 25-JAN-2001 (first entry)
XX
DE Pinus radiata transcription factor DNA sequence #106.
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KW Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
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KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
KW type 2 Cys2His2; CCAAT box element; MYB; ss.
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PF 09-MAR-2000; 2000WO-US06112.
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PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Wood M, McGrath A, Shenk MA, Glenn M;
XX
DR WPI; 2000-579369/54.
XX
PT New isolated polynucleotide encoding a plant transcription factor for
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
PT having modified gene expression or modified activity of a polypeptide
XX
PS Claim 1; Pages 158-159; 747pp; English.
XX
CC The present invention relates to novel plant transcription factors from
CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding
CC sequence for one such transcription factor. The transcription factor may
CC be used to produce a plant having modified gene expression such as a
CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
CC mahogany species or to modify the activity of a polypeptide in a plant.
CC The transcription factors of the present invention are members from the
CC following families of regulatory proteins: bZIP, bZIP family of G-box
CC binding factors, basic helix-loop-helix zipper,
CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2
CC and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements
CC and MYB.
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SQ Sequence 585 BP; 174 A; 120 C; 136 G; 155 T; 0 other;
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Job time : 259 secs

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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
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Searched: 441362 seqs, 15338381 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	41.8	4.2	2251	US-08-991-677-11	Sequence 11, Appl
6	40	4.0	3846	US-08-691-814B-3	Sequence 3, Appl
7	37.8	3.8	1000	US-09-524-168-2	Sequence 2, Appl
8	37.6	3.8	1218	US-09-134-001C-2422	Sequence 2422, Ap
9	35.8	3.6	19124	US-08-487-826B-13	Sequence 13, Appl
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19	33.8	3.4	113	US-09-054-298-23	Sequence 23, Appl
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ALIGNMENTS

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; Patent No. 6303847
; GENERAL INFORMATION:
; APPLICANT: KANAOKA, Akiyoshi
; APPLICANT: EBINUMA, Hiroyasu
; TITLE OF INVENTION: TRANSCRIPTION FACTOR CONTROLLING PHENYLPROPANOID
; FILE REFERENCE: 4859-0027-0
; CURRENT APPLICATION NUMBER: US/09/282,146A
; EARLIER FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER: JP 10-125171
; NUMBER OF SEQ ID NOS: 13
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Db 61 ACCATTGTTTGTTCCTTAACCTGCTGTATATACCATGGCTTTGACAGAACACA 120
QY 121 CAGAAATGATGCGATGTGACAGACGTATCTGTTGACAAATTAATGACAGATAAC 180
Db 121 CAGAAATGATGCGATGTGACAGACGTATCTGTTGACAAATTAATGACAGATAAC 180
QY 181 AGAATCTATACCAAAAGCTTGTTCAGATGCCATCATGCAAGGACACTGTCAAGCTTGGC 240
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Db 181 AGAATCTATCAAAAGCTTGTTCAGATGCCATCACTGCAAGGGGACATGTAAGCTTGGC 240
QY 241 AACTACATTCCTTTGAGGAGAGTCTATAGTGTAGACACACTTTGATCAGCTCTTCAAA 300
Db 241 AACTACATTCCTTTGAGGAGAGTCTATAGTGTAGACACACTTTGATCAGCTCTTCAAA 300
QY 301 CAACCTGGCAGTTGGATAAAGCTTTGAAGGTACACCAAAAATGTGAGCCACAGAAA 360
Db 301 CAACCTGGCAGTTGGATAAAGCTTTGAAGGTACACCAAAAATGTGAGCCACAGAAA 360
QY 361 CCCATTGACATGAGAAACCCAGGTAGCCAAAGTGAACCATGTTGGTGGAAACAGA 420
Db 361 CCCATTGACATGAGAAACCCAGGTAGCCAAAGTGAACCATGTTGGTGGAAACAGA 420
QY 421 GAGAAATGTTTGGCTGCAAGAAAACGTCTACCCACAGAAAAGTGTACGCCAATGGC 480
Db 421 GAGAAATGTTTGGCTGCAAGAAAACGTCTACCCACAGAAAAGTGTACGCCAATGGC 480
QY 481 AGCCCATACCATTAAGAGCTGCTTCCATGACGCCACGAGGCTGTATTAAGCCCTTCC 540
Db 481 AGCCCATACCATTAAGAGCTGCTTCCATGACGCCACGAGGCTGTATTAAGCCCTTCC 540
QY 541 AACTATACCGCATGAGGGGCGCTTATATGTAAACATCCATTCATCACTATACAG 600
Db 541 AACTATACCGCATGAGGGGCGCTTATATGTAAACATCCATTCATCACTATACAG 600
QY 601 GAGAAAGGCAACTTAAGCAAGCTTGAGGGTGACCATGAATGATTCACAGCAACAACA 660
Db 601 GAGAAAGGCAACTTAAGCAAGCTTGAGGGTGACCATGAATGATTCACAGCAACAACA 660
QY 661 GGAATCTAGCAGAGTCAATACACAGCCGACCAAGTGAATGATTCATTCACCGGGA 720
Db 661 GGAATCTAGCAGAGTCAATACACAGCCGACCAAGTGAATGATTCATTCACCGGGA 720
QY 721 TCATGTATTCAGTATGCTGCTGTAGTGTGAAGATCGAAGGCGTTCAGACACTCCATGA 780
Db 721 TCATGTATTCAGTATGCTGCTGTAGTGTGAAGATCGAAGGCGTTCAGACACTCCATGA 780
QY 781 ATGCACTTGGCTGCCAGAGGTATGTTTACTTAATCTGATTCATTAATTTGATGT 840
Db 781 ATGCACTTGGCTGCCAGAGGTATGTTTACTTAATCTGATTCATTAATTTGATGT 840
QY 841 TGAACCTATATATGCTAGCTTTTGTGTGATGATTTTGAACCTTTGTTGCTGTCTTC 900
Db 841 TGAACCTATATATGCTAGCTTTTGTGTGATGATTTTGAACCTTTGTTGCTGTCTTC 900
QY 901 ACTGTATTTATGTAATGTTGAATGATGATTAACATGTTTGGCTGCCAGTGC 960
Db 901 ACTGTATTTATGTAATGTTGAATGATGATTAACATGTTTGGCTGCCAGTGC 960
QY 961 ATGCAAATCTTTGAGCGCGCGCAATTC 988
Db 961 ATGCAAATCTTTGAGCGCGCGCAATTC 988

RESULT 2
US-08-934-627B-1
Sequence 1, Application US/08934627B
Patent No. 6169174

GENERAL INFORMATION:
APPLICANT: OSAMU HASEGAWA
APPLICANT: SATOSHI AOTSUKA
APPLICANT: SOICHIRO TAKENISHI
APPLICANT: HIROFUMI UCHIMIYA
TITLE OF INVENTION: COTTON PLANT GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 3424 Peachtree Road, N.E., 2400 Monarch Tower
CITY: Atlanta
STATE: Georgia
COUNTRY: USA

ZIP: 30326
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentlin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,627B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Roger T. Frost
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 2011-0010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 949-2400
TELEFAX: (404) 949-2499
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1015
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Gossypium hirsutum L.
FEATURE:
NAME/KEY: CDS
LOCATION: 134..757
US-08-934-627B-1

Query Match 29.0%; Score 286.8; DB 4; Length 1015;
Best Local Similarity 71.4%; Pred. No. 2.1e-78;

Matches 394; Conservative 0; Mismatches 152; Indels 6; Gaps 1;

QY 102 GGCCTTTTCAGAGAACACACAGAAATGCATGTCAGACAAAGCTGTCTATCTGTTGA 161
Db 139 GACATTCOAAGAACTCAACAAAATGCAATGCATGCACAAAGCTGTTATGCGTGA 198
QY 162 CAATTTACGTCAGATTAACAGATCTATCAACAAAGCTTTTCAGATCCATCTGCAA 221
Db 199 TAACTTACCGCTGATATAGGCTTTTCATTAAGGCTTCCGTCGACCACTTGCAA 258
QY 222 GGCACGTCAAGCTTGGCAACTCAATTCCTTGAAGGAGTCTATAGCTAGACACA 281
Db 259 GGGTACCCTCAAGCTTAGCACTACAACTCATTTGAAAGGGGTGCTATAGTGCAGCCACA 318
QY 282 CTTTGATCAGCTCTTCAACAAACTGCGAGTTTGATTAAGCTTTGAAGGTACACCAA 341
Db 319 CTATGATCACTCTTCAAGGAAGTGCAGTCTTGACAAGGTTTGAAGGAACACCAA 378
QY 342 AAATGGAAGCCACAGAAACCATTTGACAGTGAAGAAACACAGGTAGCCAAAGTGACAG 401
Db 379 GGTGTCAAACTGAAAGCAAAATCGATAGAGAGTGCACTG-----AAAGTGATGAA 432
QY 402 CATGTTGGTGGGAACAAGAGAAATGTTTGGCTGCAAGAAAAGTGTCTACCAACAGA 461
Db 433 CTGCTTTGGTGGCAACAGAAAATATGCGGCTGTTCTAAGCTGCTTATATCAAAATGA 492
QY 462 AAAGGTATCAGCCATAGGACCGCATCATTAAGAGCTGCTCAATGAGCCACGAGAG 521
Db 493 GAGGTTACTGTGAATGGCAATATATCCACAGAGCTGCTTCAAGTGTACCCATGAGAG 552
QY 522 CTGTATTAAGCCCTTCCAACTATACCGCATGAGAGGCGCTTATATATGTAACATCA 581
Db 553 GTGACCATTAAGCCATCAAACTATATAGCAATGAAGTAAACTCTACAGCAAACTCA 612
QY 582 CCATATTCAACTTATCAGAGAGAGGCAACTTAAGCAAGCTTGAGGCTGACCATGAAT 641
Db 613 CCATATCAACTCTTCAGAGAGAGAAAGTAACACCACTGAGACCGAAGAGAGAA 672

APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Strylingyl Lignin in Gymnosperms
FILE REFERENCE: 50617
CURRENT APPLICATION NUMBER: US/08/991.677A
CURRENT FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: US 60/033,381
EARLIER FILING DATE: 1996-12-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 2251
TYPE: DNA
ORGANISM: Pinus taeda
US-08-991-677-11

Query Match 4.2% Score 41.8; DB 4; Length 2251;
Best Local Similarity 55.0%; Pred. No. 0.0063;
Matches 82; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 824 TTCAATTAATTTGATGTTGAACATATATATGCTAGCTTTTGTGTGATTTTGGACCT 883
DB 282 TTGTGTTATTTTGAAGTTTATATATTTTGTATATATTTTAAATAGTTAGCT 223
QY 884 TTGTGCTGCTGCTTCTGCTGCTATATGATGATGATGATGATGATGATGATG 943
DB 222 TATTATTTATTAATCTATTTTAAATTTTGTGAGAGAGGTTGATTAAGAAGTTGGA 163
QY 944 TTTTGTCTGCCAGTCATGCAATCTTT 972
DB 162 TTAAAGTGTATGTTGAAGAATTTCTTT 134

RESULT 6
US-08-691-814B-3
Sequence 3, Application US/08691814B
Patent No. 5981218
GENERAL INFORMATION:
APPLICANT: Rio, Marie-Christine
APPLICANT: Tomasetto, Catherine
APPLICANT: Basset, Paul
APPLICANT: Byrne, Jennifer
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave, NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691.814B
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,183
FILING DATE: 09-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1383.0090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3846 base pairs

TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 76..858
US-08-691-814B-3

Query Match 4.0% Score 40; DB 2; Length 3846;
Best Local Similarity 53.1%; Pred. No. 0.03; Length 3846;
Matches 85; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 124 AATGCGATGCGATGACAGACTGCTATCTGTTGACAAATTAATGACAGATACAGA 183
DB 85 AACTGCCGCCGCTGGCGCAAGATGCTATCCACAGGAGAGGAGTGTCTGATTAAG 144
QY 184 ATCTATCACAAGCTTTGTTAGATGCCATCAGTCAAGGCGACTGTCACTGGCAAC 243
DB 145 TTCTGGCATMAAGCATGCTCTCATTTGCCAGACTGCAAGATGACATGACATGAMGAC 204
QY 244 TACAATTCCTTTGAGGCGAGTCTATCTAGTACACACT 283
DB 205 TACAGGCGCTACGAGAGAGCCCTACTGCAACGACACT 244

RESULT 7
US-09-524-168-2
Sequence 2, Application US/09524168
Patent No. 6452069
GENERAL INFORMATION:
APPLICANT: Baltz, Rachel Y.
APPLICANT: Bidney, Dennis L.
APPLICANT: Huffman, Gary A.
APPLICANT: Lu, Guihua
APPLICANT: Scelongo, Christopher J.
APPLICANT: Steinmetz, Andre A.
TITLE OF INVENTION: SP3 PROMOTER AND METHODS OF USE
FILE REFERENCE: 5718-74
CURRENT APPLICATION NUMBER: US/09/524.168
CURRENT FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1000
TYPE: DNA
ORGANISM: Helianthus annuus
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(824)
NAME/KEY: misc_feature
LOCATION: (825)..(825)
OTHER INFORMATION: Transcription Start Site begins at base No. 6452069 825
NAME/KEY: CDS
LOCATION: (929)..(1000)
US-09-524-168-2

Query Match 3.8% Score 37.8; DB 4; Length 1000;
Best Local Similarity 73.8%; Pred. No. 0.07; Length 1000;
Matches 48; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 104 CTTTGCAGGAAACACAGAAATGATGCGATGACAGAGACTGTATCTGTTGACA 163
DB 936 CATTCAAGGAGAACACCAAAATGACAGAGTTTGCAGAAACCGTATTTGGTTGATA 995
QY 164 AATTA 168
DB 996 AATTA 1000

RESULT 8
US-09-134-001C-2422/c


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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-616-368A-2

Query Match
Best Local Similarity 50.6%; Score 34.8; DB 1; Length 741;
Matches 84; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 411 TGAACAAGAGAAATGTTTGGCTGCAAGAAAGTCTACCCAGAGAAAGTATC 470
DB 339 TGAAGCTGCTGAGAAAGTCTCCAGATGTCGGGATTCGTATATGCTGCCAGAGATAT 398

QY 471 AGCCAATGGCAGCCCATACCTAAGAGCTGCTTCCATGCAAGCAGAGAGCTGTAT 530
DB 399 TGAAGCTGGAAGCCCTGGCAGCAAAAGCTTTCCGATGTCAGAAAGTCTGGAGAGCT 458

QY 531 AAGCCCTTCCACTATACCGCATGAGGGGCGCTTATATTGTAA 576
DB 459 TGAATCAACAACCTGACTGAAAAGAGTGAATCTATTGTAA 504

RESULT 11
US-09-054-298-2
; Sequence 2, Application US/09054298
; Patent No. 6136953
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Haber, Edgar
; APPLICANT: Jain, Mukesh
; APPLICANT: Yel, Shaw-Fang
; TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,298
; FILING DATE: 02-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/616,368
; FILING DATE: 15-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Beattie, Ph.D., Ingrid A.
; REGISTRATION NUMBER: P-42,306
; REFERENCE/DOCKET NUMBER: 05433/022002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 741 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-054-298-2

Query Match
Best Local Similarity 50.6%; Score 34.8; DB 3; Length 741;
Matches 84; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 411 TGAACAAGAGAAATGTTTGGCTGCAAGAAAGTCTACCCAGAGAAAGTATC 470
DB 339 TGAAGCTGCTGAGAAAGTCTCCAGATGTCGGGATTCGTATATGCTGCCAGAGATAT 398
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DB 339 TGAAGCTGCTGAGAAAGTCTCCAGATGTCGGGATTCGTATATGCTGCCAGAGATAT 398
QY 471 AGCCAATGGCAGCCCATACCTAAGAGCTGCTTCCATGCAAGCAGAGAGCTGTAT 530
DB 399 TGAAGCTGGAAGCCCTGGCAGCAAAAGCTTTCCGATGTCAGAAAGTCTGGAGAGCT 458

QY 531 AAGCCCTTCCACTATACCGCATGAGGGGCGCTTATATTGTAA 576
DB 459 TGAATCAACAACCTGACTGAAAAGAGTGAATCTATTGTAA 504

RESULT 12
US-08-818-655-2
; Sequence 2, Application US/08818655
; Patent No. 6258557
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Haber, Edgar
; APPLICANT: Jain, Mukesh
; APPLICANT: Yel, Shaw-Fang
; TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,655
; FILING DATE: 14-MAR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/616,368
; FILING DATE: 15-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 741 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-818-655-2

Query Match
Best Local Similarity 50.6%; Score 34.8; DB 4; Length 741;
Matches 84; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 411 TGAACAAGAGAAATGTTTGGCTGCAAGAAAGTCTACCCAGAGAAAGTATC 470
DB 339 TGAAGCTGCTGAGAAAGTCTCCAGATGTCGGGATTCGTATATGCTGCCAGAGATAT 398

QY 471 AGCCAATGGCAGCCCATACCTAAGAGCTGCTTCCATGCAAGCAGAGAGCTGTAT 530
DB 399 TGAAGCTGGAAGCCCTGGCAGCAAAAGCTTTCCGATGTCAGAAAGTCTGGAGAGCT 458

QY 531 AAGCCCTTCCACTATACCGCATGAGGGGCGCTTATATTGTAA 576
DB 459 TGAATCAACAACCTGACTGAAAAGAGTGAATCTATTGTAA 504
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RESULT 13
US-08-616-368A-7
; Sequence 7, Application US/08616368A
; Patent No. 5767262
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-Eh
; APPLICANT: Haber, Edgar
; APPLICANT: Jain, Mukesh
; APPLICANT: Yet, Shaw-Fang
; TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/616,368A
; FILING DATE: 15-MAR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/022001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 880 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-616-368A-7

Query Match          3.5%; Score 34.6; DB 1; Length 880;
Best Local Similarity 49.2%; Pred. No. 0.63;
Matches 91; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 112 GGAACACACAGAAATGATGCGATGTGACAAAGACTGTCTATCTGTTGACAAATTAAT 171
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DB 394 GGAGGTGCTGAGAAAGTCTCCAGATGTGGGATTCGTGTATCTGCTGAGAAATCAAT 453

QY 172 GCAGATAACAGATCTATACAAAGCTTGTTCAGATGCCATCAGTGCAGAGGCACCTGTC 231
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 454 GGAGGTGAGAAAGCCCTGGACAAAACTGTTCCGATGTGCCAAGTGTGGGAAGACTCTG 513

QY 232 AAGCTTGGCACTACATTCCTTTGAGGAGTCTCTACTGTAGACCACTTTGATCAG 291
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 514 GAGTCTACAACCTGACTGAGAGGAAGGTGAATCTACTGTAAGGGTGTCTACGCAAG 573

QY 292 CTCCTT 296
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DB 574 AACTT 578
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RESULT 14
US-09-054-298-7
; Sequence 7, Application US/09054298
; Patent No. 6136953
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-Eh
; APPLICANT: Haber, Edgar

RESULT 15
US-08-818-655-7
; Sequence 7, Application US/08818655
; Patent No. 6258557
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-Eh
; APPLICANT: Haber, Edgar
; APPLICANT: Jain, Mukesh
; APPLICANT: Yet, Shaw-Fang
; TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN

APPLICANT: Jain, Mukesh
APPLICANT: Yet, Shaw-Fang
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,298
FILING DATE: 02-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/616,368
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Beattie, Ph.D., Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 05433/022002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 880 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 55...633
US-09-054-298-7

Query Match          3.5%; Score 34.6; DB 3; Length 880;
Best Local Similarity 49.2%; Pred. No. 0.63;
Matches 91; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 112 GGAACACACAGAAATGATGCGATGTGACAAAGACTGTCTATCTGTTGACAAATTAAT 171
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 394 GGAGGTGCTGAGAAAGTCTCCAGATGTGGGATTCGTGTATCTGCTGAGAAATCAAT 453

QY 172 GCAGATAACAGATCTATACAAAGCTTGTTCAGATGCCATCAGTGCAGAGGCACCTGTC 231
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 454 GGAGGTGAGAAAGCCCTGGACAAAACTGTTCCGATGTGCCAAGTGTGGGAAGACTCTG 513

QY 232 AAGCTTGGCACTACATTCCTTTGAGGAGTCTCTACTGTAGACCACTTTGATCAG 291
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 514 GAGTCTACAACCTGACTGAGAGGAAGGTGAATCTACTGTAAGGGTGTCTACGCAAG 573

QY 292 CTCCTT 296
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DB 574 AACTT 578
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2002, 23:02:28 ; Search time 57 Seconds

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Title: US-09-928-412-1

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Gapop 10.0 , Gapext 1.0

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 671156

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	988	100.0	988	US-09-928-412-1	Sequence 1, Appli
2	295.4	29.9	744	US-09-770-149-39	Sequence 39, Appli
3	197.4	20.0	418	US-09-878-574-30	Sequence 30, Appli
4	192.2	19.5	396	US-09-878-574-3019	Sequence 3019, Ap
5	141.6	14.3	693	US-09-770-149-291	Sequence 291, App
6	132.2	13.4	345	US-09-878-574-22	Sequence 22, Appli
7	108.2	11.0	391	US-09-878-574-458	Sequence 458, App
8	100.2	10.1	378	US-09-878-574-1429	Sequence 1429, Ap
9	96.4	9.8	373	US-09-878-574-964	Sequence 964, App
10	94.2	9.5	405	US-09-878-574-3948	Sequence 3948, Ap
11	89.6	9.1	264	US-09-878-574-14576	Sequence 14576, A
12	83.6	8.5	280	US-09-294-093B-3904	Sequence 3904, Ap
13	82	8.3	279	US-09-294-093B-4538	Sequence 4538, Ap
14	79.4	8.0	296	US-09-878-574-3381	Sequence 3381, Ap
15	78.2	7.9	1081	US-09-880-192-13	Sequence 5, Appli
16	78	7.9	2379	US-09-880-192-13	Sequence 13, Appli
17	78	7.9	3336	US-09-833-381-1727	Sequence 1727, Ap
18	74	7.5	330	US-09-294-093B-3580	Sequence 3580, Ap
19	73.2	7.4	397	US-09-789-919-41	Sequence 41, Appli

20	71.6	7.2	732	10	US-09-925-297-152	Sequence 152, App
21	71.6	7.2	2749	10	US-09-822-849A-399	Sequence 399, App
22	70.2	7.1	743	10	US-09-789-919-6	Sequence 6, Appli
23	66	6.7	276	10	US-09-878-574-13619	Sequence 13619, A
24	63.8	6.5	705	10	US-09-833-381-1735	Sequence 1735, Ap
25	63.8	6.5	1299	10	US-09-833-381-1733	Sequence 1733, Ap
26	63.4	6.4	541	10	US-09-833-381-1730	Sequence 1730, Ap
27	52.2	5.3	623	10	US-09-833-381-1736	Sequence 1736, Ap
28	46.4	4.7	355	10	US-09-770-791-626	Sequence 626, App
29	43.2	4.4	276	10	US-09-878-574-14665	Sequence 14665, A
30	41.8	4.2	2251	10	US-09-796-256A-11	Sequence 11, Appli
31	40.8	4.1	167	10	US-09-294-093B-3953	Sequence 3953, App
32	40.8	4.1	738	10	US-09-910-943-6	Sequence 6, Appli
33	40	4.0	1273	10	US-09-773-926-1	Sequence 1, Appli
34	40	4.0	1273	10	US-09-773-926-2	Sequence 2, Appli
35	40	4.0	1273	10	US-09-773-926-3	Sequence 3, Appli
36	37.4	3.8	288	10	US-09-924-093B-4931	Sequence 4931, App
37	37.2	3.8	248	10	US-09-923-876-5837	Sequence 5837, Ap
38	36.8	3.7	413	10	US-09-960-352-2919	Sequence 2919, Ap
39	36.4	3.7	84539	10	US-09-962-436-36	Sequence 36, Appli
40	35.2	3.6	406	10	US-09-960-352-10265	Sequence 10265, A
41	35	3.5	1938	10	US-09-841-132-532	Sequence 532, App
42	34.8	3.5	237	10	US-09-960-352-14543	Sequence 14543, A
43	34.8	3.5	385	10	US-09-960-352-1739	Sequence 1739, Ap
44	34.8	3.5	1084	9	US-09-938-842A-3786	Sequence 3786, Ap
45	34.8	3.5	2000	10	US-09-887-576-143	Sequence 143, App

ALIGNMENTS

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RESULT 1
US-09-928-412-1
: Sequence 1, Application US/09928412
: Patent No. US20020123623A1
:
: GENERAL INFORMATION:
: APPLICANT: KAWAKA, Akiyoshi
: APPLICANT: EBINUMA, Hiroyasu
: TITLE OF INVENTION: TRANSCRIPTION FACTOR CONTROLLING PHENYLPROPANOID
: FILE REFERENCE: BIOSYNTHESIS PATHWAY
: CURRENT APPLICATION NUMBER: 4859-0027-0
: CURRENT FILING DATE: 2001-08-14
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/928,412
: PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 10-125171
: PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-31
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: PatentIn Ver. 2.1
:
: SEQ ID NO 1
: LENGTH: 988
: TYPE: DNA
: ORGANISM: Nicotiana tabacum
:
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (100)..(702)
: NAME/KEY: misc.feature
: LOCATION: (127)..(282)
: OTHER INFORMATION: LIM domain
: NAME/KEY: misc.feature
: LOCATION: (427)..(582)
: OTHER INFORMATION: LIM domain
US-09-928-412-1
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Query Match 100.0% ; Score 988 ; DB 10 ; Length 988 ;
Best Local Similarity 100.0% ; Pred. No. 2.1e-260 ;
Matches 988 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

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QY 1 GAATTCGCGCCGTTCCAAAACCAAGTGTACACAAAGGAAGGACGACCAAG 60
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Db 1 GAATTCGCGCCGTTCCAAAACCAAGTGTACACAAAGGAAGGACGACCAAG 60
QY 61 ACCATTTTGTTCGTATAAAGTCTGCTATATAGCCATGCGCTTTTCAGAGACCA 120
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Db 61 ACCATTTTGTCTCTGTAACCTTGCCTGATATAGCATAGGCTTTGCGAGAACACA 120
QY 121 CAGAAATGCATGCGATGACAGATGCTATCTGTTGGTGAACAATTAACTGCAATTAAC 180
Db 121 CAGAAATGCATGCGATGACAGATGCTATCTGTTGGTGAACAATTAACTGCAATTAAC 180
QY 181 AGAATCTATCAACAAGCTTTGTTGAGATGCCATCCTGCAAGGGCAGCTGTCAAGCTTGGC 240
Db 181 AGAATCTATCAACAAGCTTTGTTGAGATGCCATCCTGCAAGGGCAGCTGTCAAGCTTGGC 240
QY 241 AACTACATTTCTTTGAGGAGTCTATCTGTTGAGCAGCAGCTTTGATCAGCTTTTCAA 300
Db 241 AACTACATTTCTTTGAGGAGTCTATCTGTTGAGCAGCAGCTTTGATCAGCTTTTCAA 300
QY 301 CAAATCTGCGATTTGATTAAGGTTGAAAGGTACACCAAAAATGTAAGGCCACAGAAA 360
Db 301 CAAATCTGCGATTTGATTAAGGTTGAAAGGTACACCAAAAATGTAAGGCCACAGAAA 360
QY 361 CCCATTTGACAGTGAAGAACACAGATGAGCCAAAGTGAACAGATGTTTGTGTAACAGA 420
Db 361 CCCATTTGACAGTGAAGAACACAGATGAGCCAAAGTGAACAGATGTTTGTGTAACAGA 420
QY 421 GAGAAATGTTTGGCTGCAAGAAATCTGTACCCACAGAAAAGGTATCAGCCAAATGCC 480
Db 421 GAGAAATGTTTGGCTGCAAGAAATCTGTACCCACAGAAAAGGTATCAGCCAAATGCC 480
QY 481 ACAGCATACCATTAAGAGCTCTTCCATGACAGCCAGGAGCTGTGTAATAGCCCTTCC 540
Db 481 ACAGCATACCATTAAGAGCTCTTCCATGACAGCCAGGAGCTGTGTAATAGCCCTTCC 540
QY 541 AACTATACCGACATGAGGGGCGCTTATATTTGTAACATCAACATTAATCAACTATCAAG 600
Db 541 AACTATACCGACATGAGGGGCGCTTATATTTGTAACATCAACATTAATCAACTATCAAG 600
QY 601 GAGAGGGGCAACTTAACAGAGCTTGAGGGTACCATGAATGATTCACAGACAGACACA 660
Db 601 GAGAGGGGCAACTTAACAGAGCTTGAGGGTACCATGAATGATTCACAGACAGACACA 660
QY 661 GGAATCTGACAGATGATACAGAGCCGACCAAGTATGATTCCTTATCCGCGA 720
Db 661 GGAATCTGACAGATGATACAGAGCCGACCAAGTATGATTCCTTATCCGCGA 720
QY 721 TCATGATTAACGATGCTGCTTGTAGTGTGAAGATGCAAGGCGCTTGACAGCTTCCATGA 780
Db 721 TCATGATTAACGATGCTGCTTGTAGTGTGAAGATGCAAGGCGCTTGACAGCTTCCATGA 780
QY 781 ATGCACTTGGCTTGGCCGACGATGTTTACCTATACCTTACCTTCAATTAATTTGATGT 840
Db 781 ATGCACTTGGCTTGGCCGACGATGTTTACCTATACCTTACCTTCAATTAATTTGATGT 840
QY 841 TGAATATATATTTGCTAGCTTTTGTGTAGATTTTGGACCTTTGCTTGTGCTTGC 900
Db 841 TGAATATATATTTGCTAGCTTTTGTGTAGATTTTGGACCTTTGCTTGTGCTTGC 900
QY 901 ACTTGTATTAATGGAATGTTGAATGAGATGAATTAACAGGCTTTGCTGCTCCAGTGC 960
Db 901 ACTTGTATTAATGGAATGTTGAATGAGATGAATTAACAGGCTTTGCTGCTCCAGTGC 960
QY 961 ATGCAATCTTTGAGGCGCGCGCAATTC 988
Db 961 ATGCAATCTTTGAGGCGCGCGCAATTC 988

RESULT 2

US-09-770-149-39
; Sequence 39, Application US/09770149
; Patent No. US2002005963A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.

APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Mathew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Moessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krieger, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: thaliana
CURRENT APPLICATION NUMBER: us/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 39
LENGTH: 744
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-770-149-39

Query Match 29.9%; Score 295.4; DB 10; Length 744;
Best Local Similarity 75.3%; Pred. No. 3, 2e-71;
Matches 368; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 143 AGACTGCTATCTGCTGTAACAAATTAACCTGACATTAACAAATCTATCAACAAGCTTGT 202
Db 1 AAACAGTTTATCTTGTGCAAGATTTACCGCGATTAACCGGCTACCAACAAGCTTGT 60
QY 203 TCAGATGCCATCACTGCAAGGCACTGTCAAGCTTGCAACTGCAATTCCTTTGAGGAG 262
Db 61 TCCGATGTCCACATTTGCAAGGAACCTCTCAAGCTTGAATTAACACTCTTTGAGGAG 120
QY 263 TTCTATCTGTAACCAACACTTGTATGATGCTTTCAAAACAAGCTTGTGATTA 322
Db 121 TTCTATCTGTAACCAACACTTGTATGATGCTTTCAAAACAAGCTTGTGATTA 180
QY 323 GCTTGAAGGTACCAAAAATGTAAGGCCACAGAAACCATTTGACATGAGAAACAC 382
Db 181 GCTTGAAGGTACCAAAAATGTAAGGCCACAGAAACCATTTGACATGAGAAACAC 240
QY 383 AGGTAGCCAAAGTGAACAGCATTTTGTGTAACAGAGAAATGTTTGGCTGCAAGA 442
Db 241 CTGGAACCAAGTTTGAATATTTTGTGTAACAGAGAAATGTTTGGCTGCAAGA 300
QY 443 AAACCTGTTACCAAGAAAGATATCAAGCCAAATGAGCCCAATACATTAAGAGCTGCT 502
Db 301 AAACCTGTTACCAAGAAAGATATCGGTGAATGAGCAATTTACCAAGAGCTGCT 360
QY 503 TCCAAAGCAAGCCAGAGGCTGTGTAAATGAGCCCTTCCAACTTACCAGCATGAGAGGGC 562
Db 361 TCAAGGTACACATGAGAGGCTGTGTAAATGAGCCCTTCCAACTTACCAGCATGAGAGGGC 420
QY 563 GCTTATATTTGAACATCAACATATTTCAACTTTCAAGGAGAAAGGCACTTAAGCAAGC 622
Db 421 AGCTATATTTGAACATCAACATATTTCAAGTGTATCAAGGAGAAAGAACTTGAGGCAAGC 480
QY 623 TTGAGGAGTG 631
Db 481 TCGAAGGAG 489

RESULT 3

US-09-878-574-30


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; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1429
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-037-Q1-B1-G7
US-09-878-574-1429
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Query Match          10.1%; Score 100.2; DB 10; Length 378;
Best Local Similarity 66.4%; Pred. No. 4.9e-18;
Matches 144; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
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QY 98 CCATGCGTTTGCAGACACACACAGAAATGCATGCGATGACAGACTGCTATCTGG 157
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DB 151 CAATGTCATTACACAGAACTACAGTAAATGCAAGGCTTGATTAAGACTGTTATGTGG 210
QY 158 TTGACAAATTAATCTGCAGATATACAGATCTATCACAAGCTTGTTCAGATGCATCACT 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 211 ATGACATGTGAATCTTTGAAGGTATACCTTACCATAGAACTGCTTACATGACATGACT 270
QY 218 GCAAGGGCACTGTCAAGCTTGGCACTACAATTCCTTTGAGGAGTTCTATCTAGTAGAC 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 271 GCAAGGAGTACCGACAGATGATACCTACGCCACAGATGATGTGCTCTATTTGCAAGC 330
QY 278 CACACTTTGATCAGCTCTTCAACAAACTGGCGATT 314
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DB 331 CACACTTTGAAACGCTTTTCAAGAACTGTGCAATTT 367
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RESULT 9
US-09-878-574-964
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; Sequence 964, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Thompson, Michael J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 964
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(373)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3028-044-Q1-B1-B10
US-09-878-574-964
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Query Match          9.8%; Score 96.4; DB 10; Length 373;
Best Local Similarity 66.2%; Pred. No. 5.3e-17;
Matches 139; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
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QY 100 ATGCGTTTTCAGAGACACACAGAAATGCATGCGATGTACAGAGCTGCTATCTGGTT 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 115 ATGCGATTTCAGCGGAGCCCAAGAAATGCAAGCTTGCACAAAACCTGTTCACCTTGTC 174
QY 160 GACAAATTAATCTGCAGATATACAGATCTATCACAAGCTTGTTCAGATGCATCACTGCG 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 175 GAAGGTTTATCTGCTGATGGGCTGCTTATCACAAGAAATGCTTCAATGACGACCATTCG 234
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QY 220 AAGGCACTGTCAAGCTTGGCAACTACAAATTCCTTTGAGGAGTCTATACGTAGACCA 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 235 AATGGCCTCTGCGAATACCACTACTCATCCAGCAAGGGTTTGTACTGCAAGGTG 294
QY 280 CACTTTGATCAGCTCTTCAACCAACTGCG 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 295 CACTTTGAGCAGCTTTTCAAGAAACTGCG 324
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RESULT 10
US-09-878-574-3948
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; Sequence 3948, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Thompson, Michael J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3948
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-003-Q1-B1-E7
US-09-878-574-3948
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Query Match          9.5%; Score 94.2; DB 10; Length 405;
Best Local Similarity 65.4%; Pred. No. 2.2e-16;
Matches 138; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
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QY 100 ATGCGTTTTCAGAGACACACAGAAATGCATGCGATGTACAGAGCTGCTATCTGGTT 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 115 ATGCGATTTCAGCGGAGCCCAAGAAATGCAAGCTTGCACAAAACCTGTTCACCTTGTC 174
QY 160 GACAAATTAATCTGCAGATATACAGATCTATCACAAGCTTGTTCAGATGCATCACTGCG 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 175 GAAGGTTTATCTGCGGATGAGCTGCTTATCACAAGAACTGCTCAATGACGACCATTCG 234
QY 220 AAGGCACTGTCAAGCTTGGCAACTACAAATTCCTTTGAGGAGTCTATACGTAGACCA 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 235 AATGGCCTCTTGCAGATACCACTACTCATCCAGCAAGAGTTTGTACTGCAAGGTG 294
QY 280 CACTTTGATCAGCTCTTCAACCAACTGCGA 310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 295 CACTTTGAGCAGCTTTTCAAGAAACTGGA 325
```

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RESULT 11
US-09-878-574-14576
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; Sequence 14576, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Thompson, Michael J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 14576
; LENGTH: 264
; TYPE: DNA
; ORGANISM: Glycine max
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[illegible]

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RESULT 14
US-09-878-574-3381
; Sequence 3381, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 381
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-011-Q1-B1-G8
US-09-878-574-3381

Query Match      8.0%; Score 79.4; DB 10; Length 296;
Best Local Similarity 66.9%; Pred. No. 2.1e-12;
Matches 113; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 22, 2002, 22:12:03 ; Search time 1964 Seconds

(without alignments)
8147.220 Million cell updates/sec

Title: US-09-928-412-1

Perfect score: 988
1 gaattcgcgccgttccaaa.....cttgagcgcgccgaattc 988

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
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16: em_estom:*
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18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	381.2	38.6	537	14	BQ115637 EST601213
2	361.8	36.6	755	9	AJ498553 AJ498553
3	361.6	36.6	714	14	BU014288 BU014288
4	361.6	36.6	740	14	BU008321 BU008321
5	360.2	36.5	645	14	BQ148732 BQ148732
6	360	36.4	690	14	BO857598 BO857598

7	358.6	36.3	782	10	AM559538
8	344.4	34.9	698	10 <td>BE203860</td>	BE203860
9	333.2	33.7	538	13 <td>B1129342</td>	B1129342
10	330.4	33.4	593	12 <td>BC043927</td>	BC043927
11	326.8	33.1	548	10 <td>BE440655</td>	BE440655
12	313.2	31.7	589	14 <td>BO741219</td>	BO741219
13	312.4	31.6	656	14 <td>BO623451</td>	BO623451
14	310.2	31.4	657	12 <td>BF638624</td>	BF638624
15	309.6	31.3	585	13 <td>BM178858</td>	BM178858
16	309	31.3	531	12 <td>BF425662</td>	BF425662
17	302.6	30.6	553	10 <td>BE210592</td>	BE210592
18	300.8	30.4	503	12 <td>BC362712</td>	BC362712
19	298.8	30.2	548	10 <td>AW761298</td>	AW761298
20	298.4	30.2	571	10 <td>AM559283</td>	AM559283
21	297.8	30.1	531	10 <td>BE473593</td>	BE473593
22	295.6	29.9	527	14 <td>BO785792</td>	BO785792
23	295	29.9	580	10 <td>AV831505</td>	AV831505
24	294.4	29.8	631	14 <td>BO628770</td>	BO628770
25	292.4	29.6	647	12 <td>BG138218</td>	BG138218
26	289.2	29.3	514	9 <td>A1930682</td>	A1930682
27	287	29.0	471	13 <td>BM173395</td>	BM173395
28	286	28.9	693	13 <td>BM301553</td>	BM301553
29	282.6	28.6	950	11 <td>AY112454</td>	AY112454
30	282.2	28.6	624	14 <td>BO048239</td>	BO048239
31	282	28.5	641	14 <td>BQ134245</td>	BQ134245
32	281	28.4	585	12 <td>BG156003</td>	BG156003
33	280.2	28.4	543	14 <td>BO514084</td>	BO514084
34	279	28.2	506	13 <td>BM143254</td>	BM143254
35	275.6	27.9	561	13 <td>BM178019</td>	BM178019
36	271	27.4	647	14 <td>BO279385</td>	BO279385
37	271	27.4	670	13 <td>BM299814</td>	BM299814
38	270.2	27.3	599	14 <td>BU037830</td>	BU037830
39	268.6	27.2	536	13 <td>B1417129</td>	B1417129
40	268.6	27.2	536	13 <td>B1674161</td>	B1674161
41	268.6	27.2	667	12 <td>BC454148</td>	BC454148
42	268.2	27.1	846	14 <td>BO752856</td>	BO752856
43	267.8	27.1	559	12 <td>BF146081</td>	BF146081
44	266.6	27.0	655	10 <td>BE443538</td>	BE443538
45	266.4	27.0	632	12 <td>BG140591</td>	BG140591

ALIGNMENTS

RESULT 1
LOCUS BQ115637 537 bp mRNA linear EST 22-JUL-2002
DEFINITION EST601213 mixed potato tissues Solanum tuberosum cDNA clone STMC51
5' end, mRNA sequence.
ACCESSION BQ115637
VERSION BQ115637.2 GI:21917057
KEYWORDS EST
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 537)
REFERENCE Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C.,
Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and
Karamycheva,S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished (2002)
On Apr 17, 2002 this sequence version replaced gi:20167599.
CONTACT: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potatodtgr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
cdna@resgen.com
Seq primer: T3.
Location/Qualifiers

FEATURES

Query Match	Best Local Similarity	Matches	Conservative	Score	DB	Length
Query Match	84.4%	444	0	381.2	DB 14	537
				Pred. No. 1.3e-83		
				Mismatches 73	Indels 9	Gaps 1
BASE COUNT	187 a	103 c	113 g	134 t		
ORIGIN						
1	537					
/organism="Solanum tuberosum"						
/cultivar="Kennebec or Blinje"						
/db_xref="taxon:4113"						
/clone="STMD051"						
/clone.lib="mixed potato tissues"						
/tissue_type="mixed tissues"						
/lab_host="SOLR"						
/note="vector: pBluescript SK(-); Site.1: EcoRI; Site.2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes 'tubers, or roots.'"						
Query Match	84.4%	444	0	381.2	DB 14	537
Best Local Similarity	84.4%	444	0	381.2	DB 14	537
Matches	444	Conservative	0	Mismatches	73	Indels 9
						Gaps 1
BASE COUNT	187 a	103 c	113 g	134 t		
ORIGIN						
1	537					
/organism="Solanum tuberosum"						
/cultivar="Kennebec or Blinje"						
/db_xref="taxon:4113"						
/clone="STMD051"						
/clone.lib="mixed potato tissues"						
/tissue_type="mixed tissues"						
/lab_host="SOLR"						
/note="vector: pBluescript SK(-); Site.1: EcoRI; Site.2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes 'tubers, or roots.'"						

TITLE	JOURNAL	COMMENT	FEATURES
Linke, B., Puelhler, A. and Kuester, H.			
Determination of transcript sequences from developing pods			
Including seeds of Medicago truncatula genotype A17			
Unpublished (2002)			
Contact: Kuester H			
Lehrstuhl fuer Genetik			
Universitaet Bielefeld			
Postfach 100131, D-33501 Bielefeld, Germany.			
Location/Qualifiers			
1. .755			
/organism="Medicago truncatula"			
/db_xref="taxon:3880"			
/clone="mt-acc955206a09"			
/clone_lib="MPPOSE"			
/tissue_type="pods including seeds"			
/dev_stage="different stages of development"			
/note="vector: pGEM-T; Site_1: PstI; Site_2: SphI;			
genotype A17: cDNA was prepared from polyA+ enriched RNA			
from developing pods including seeds harvested at			
different stages of development. The cDNA was			
directionally ligated by Medigenomix into the pGEM-T			
vector from Promega using GCGAGCGCGCGAGCGCGCGCAGC and			
CAGCAGCGCATATGCGCGCGG adapters. Plasmids containing cDNA			
inserts were propagated in E. coli DH10B cells."			
BASE COUNT	252 a	136 c	150 g
ORIGIN			217 t
Query Match	36.6%	Score 361.8;	DB: 9; Length 755;
Best Local Similarity	77.5%;	Pred. No. 8.4e-79;	
Matches 436; Conservative	0;	Mismatches 127;	Indels 0; Gaps 0

QY	100	ATGGCTTTTTCAGAGAACACACAGAAATCATGCGCATGTGCAAGACATGCTATCTGGT	159
Db	113	ATGGCAATTCGAGGAACAACTCGAAGTGTATGGCTTGTAAACAAAGCTTATCTGGT	172
QY	160	GACAAATTAACCTGACATACAGATCTATCTACAAAGCTTGTTCAGATGCCATCTACTGC	219
Db	173	GATTAAGTTAACTGCTATATAATGAAATTTTCCAAAGCTTGTTCAGATGTCACACTGCG	232
QY	220	AAGGGCACTGTCAAGCTGGCAACTCATCTCTTGTGAGGGAGTGTCTATCTGTAGACCA	279
Db	233	AAAGGAACCTCTCAAGCTAAGCAACTATCAATTTCTTTTGAAGGAGTTCCTTACTGCAAGCA	292
QY	280	CACTTTGGATCAGCTCTCTCAAAACAACCTGGCAGTTTGGATAAAGCTTTGAAGGTACACA	339
Db	293	CACCTTCACCAACTGTTTCAAAAGAACTGGTACTGTCCTTGAAGAAACCTTTGAAGGACACCG	352
QY	340	AAAAATGTGAGGCACAGAAACCCANTGCACTGTGAAGAACCAACAGGTATGCCAAAGTACA	399
Db	353	AAAATGTCTCAGGCGCAAAAGAAATATAGTAAATGTGAAGAACTGCTGCACGAAAGGCTTCA	412
QY	400	AGCATGTTTGGTGGAAACAAGAGAGAAATGTTTTGGCTGCTCAAGAAACACTGTTCTACCACACA	459
Db	413	AGTATGTTTGGTGGAAACAAGGACAAATGTCTGGTTGTCAGAAACAGTATCCACAAT	472
QY	460	GAAAGGTATCAGCCAAATGGCACGCCATACCTTAAGAACTCTCTTCATATGACGACGGGA	519
Db	473	GAGAAAGTTACAATGATGAATGAAACTCTTAAACCAATAGAGTCTTTCAAATGTGGTCATAGGA	532
QY	520	GGCGTGTATTAAGCCCTTCCAACTATACCCGACATGAGGGGCGCTCTATATATTGAAACAT	579
Db	533	GGGTGTACATATCAGTCTCTTCCAAATTACATAGACACATGAGGGGAAAAATTTCTATCGAAACAC	592
QY	580	CACCATATTCACATTATACAGAGAGAGGGCACTTAAAGCAAGCTTGAAGGCTGACCATGAA	639
Db	593	CACCATATTCACATGATGTCAAGCAAAAAGGAAATTTAAAGCCAGCTAGAAGGTGACCATGAG	652
QY	640	ATGATTTTCCAGCAGCAACACAGAG 664	
Db	653	AAAAATGCTGGGAAAAATCATGTGTG 677	

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
BUT014288						
LOCUS	BUT014288	714 bp	mRNA	linear	EST 22-AUG-2002	
DEFINITION	OG6P01.yg.ab1 OG_FERGU lettuce serritola Lactuca sativa cDNA clone					
ACCESSION	OG6P01, mRNA sequence.					
VERSION	BUT014288					
KEYWORDS	BUT014288.1 GI:22448683					
SOURCE	EST.					
ORGANISM	Lactuca sativa. Lactuca sativa Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterales; euasterids II; Asterales; Asteraceae; Lactuceae; Lactuca.					
REFERENCE	1 (bases 1 to 714)					
AUTHORS	Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,W., Lavelle,D., Chevalier,P., Ziegler,J., Ellison, 'P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lal,Z., Church,S., Jackson,L. and Birdford,K. Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/ Unpublished (2002) Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel.: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu] belongs to contig OG_Ca_Conflig6843, see http://cgpsdb.ucdavis.edu/ for details.					
JOURNAL COMMENT						
TITLE						
row=	OG6P	p	column=	01.		

	FEATURES	
	source	
	Location/Qualifiers	
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	/cultivar="L.serricola"	
	/db_xref="taxon:4236"	
	/clone="OgJ6P01"	
	/clone_1id="OG_EFGH lettuce serricola"	
	/lab_host="E.coli"	
	/note="Vector: pBRcDNASfIAB: The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformed into a custom medium-copy vector to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cpdpd.ucdavis.edu/TAG_LIB-OG_EFGH lettuce serricola	
	TAG_TISSUE=flowers pre-fertilized	
	TAG_SEQ=GCTTGACGGC"	
BASE COUNT	209 a 161 c 151 g 193 t	
ORIGIN		
Query Match	36.6%	Score 361.6; DB: 14; Length 714;
Best Local Similarity	81.0%;	Pred. No. 9.3e-79;
Matches 421:	Conservative 0; Mismatches 99; Indels 0; Gaps 0;	
OY 115	ACCACACAGAATGATGCATGTGCACAAGCTGTCTATTGTTGACAAATAACTGCA	174
Db 1	ACAAACCAGAAATGATGATGGCATGTGCACAAGCTGTCTACCTGGTGAACAACCTCA	60
OY 175	GATAACAGATCTATCACAAAGCTTGTTTCAGATGCCATCACTGCAGGCACTGTCAAG	234
Db 61	GATATATCCATCTTCACAAAAGCTTGCTTCAGATGCCACATTGCAAGGCAACCTCAAG	120
OY 235	CTTGCGAACCTCAATATCTTGGAGGAGATTTCATACCTTAGACCAACACTTTGATCAGCT	294
Db 121	CTTAGCAACTCAACTCTCTTTGAGGGAATTCGTATTTCACAGGCCACACTTTGATCACTC	180
OY 295	TTTCAACAACAAGCTGCAGTTTGGATTAAGAAGCTTTGAAGGTACACCAAAAAATGTGAAGCA	354
Db 181	TTTCAAGAAGACTGGTAGCTTAGACAAAAGCTTTGAAGGCACCAAAATATTTTGAAGCA	240

OY	355	CAGAAACCATTGACGTGAGAAAACCAAGGTAGCAGAAGTGAACATCTTTGGTGA	414
Db	241	CAGAAAACCATTTGATGTGTGAGAAACCAATGGCTAACAAAGATATCTAGCATGTTTGSTGGG	300
OY	415	ACAAGAGAGAAATGTTTTGGCTGCAGAAAACTGTCTACCCACAGAAAAAGTATCACCC	474
Db	301	ACCACAGATTAATGTTTGGCTGCAGAAAAACCGCTTCACACAGAAAAGTTTCACATA	360
OY	475	AATGCCACGCATCCATTAAGAGGTGCTTCCAATGSCACCCAGGAGGCTGTGTATATAGC	534
Db	361	AATGGAACCTTATACCAAAAGCTGCTTCAAAGTATATCTATGGAGGATGTGTGATCAGC	420
OY	535	CGTTCCAACTTATACGCAACATGAGGGGGCTTATATTTGTAACATCACCATATTCAACTT	594
Db	421	CCATCAACCTATTATGACATGAAGAGTGGCTCTACTGACAGACACACACCACTCACTC	480
OY	595	ATCAAGAGAAAGGCAACTTAAGCAAGTTGAGGTGAGCC	634
Db	481	ATCAGAGAAAGGTAACTTGCCAGCTGCAAGGGGTGAGCC	520

RESULT 4	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	COMMENT
B0008321		B0008321								
		740 bp mRNA Linear EST 22-AUG-2002								
		OG67D23.Yg.abl OG_EFGH lettuce serriola Lactuca sativa cDNA clone								
		OG67D23, mRNA sequence.								
		B0008321								
		B0008321.1 GI:22442716								
		EST.								
		Lactuca sativa.								
		Lactuca sativa								
		Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
		Spermatophyta; Magnoliophyta: eudicotyledons; core eudicots;								
		Asteridae; easterids II; Asterales; Asteraceae; Lactuceae;								
		Lactuca.								
		1 (bases 1 to 740)								
		Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,								
		Lih,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison								
		,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,								
		Church,S., Jackson,L. and Bradford,K.								
		Lettuce and Sunflower ESTs from the Compositae Genome Project								
		http://compgenomics.ucdavis.edu/								
		Unpublished (2002)								
		Contact: Alexander Kozik [R.W.Michelmore]								
		Department of Vegetable Crops, R.W.Michelmore Lab								
		University of California at Davis (UCD)								
		Asmundson Hall, UCD, Davis, CA 95616, USA								
		Tel: 1-(530)-742-1742								
		Fax: 1-(530)-752-9659								
		Email: akozik@ucdavis.org [michelmore@vegmall.ucdavis.edu]								
		belongs to contig OG_Ca_contig6843, see http://cspdb.ucdavis.edu/								
		for details.								
		plate: OGH7 row: D column: 23.								

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location/Qualifiers
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/cultivar="L. serriola"
/db_xref="taxon:4236"
/clone="OGF7D23"
/clone_lib="OG_ERGHJ lettuce serriola"
/lab_host="E. coli"
/note="vector: pRCNDNA5fab: The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB=OG_ERGHJ lettuce serriola
TAG_TISSUE=flowers pre-fertilized

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BASE COUNT 215 a 163 c 159 g 203 t
ORIGIN TAG-SEQ-GCTTGACGGG"
Query Match 36.6%; Score 361.6; DB 14; Length 740;
Best Local Similarity 81.0%; Pred. No. 9.4e-79;
Matches 421; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 115 ACCACACGAAATGCGATGTCACAAAGCTGTCTATCTGTTGACAAATTAAGTCGA 174
DB 2 ACACACCGAATGATGATGTCACAAAGCTGTCTATCTGTTGACAAAGTCGA 61
QY 175 GATAACAGAAATCTATACAAAGCTGTTGACAGCCATCAGAGGACACTGTCAG 234
DB 62 GATATGCGATCTTCCAAAGCTGTTGACAGCCATCAGAGGACACTGTCAG 121
QY 235 CTTGACAGCTACAAATCTGTTGAGGAGTTCTATACCTAGACCACTTTGATCAGCTC 294
DB 122 CTTAGCAACATCAACTCTCTTTGAGGAGTTCTGTTATTCAGGCCCACACTTTGATCACTC 181
QY 295 TTCAAAACAACTGCGAGTTGGATTAAGCTTTGAAGGTACACCAAAATGTGAAGCCA 354
DB 182 TTCAAAAGAGCTGCTGAGCTTAGACAAAGCTTTGAAGGCACACCAAGATTTTGAAGCCA 241
QY 355 CAGAAACCATTTGACAGTGACAAACACAGTAGCCAAAGTGACAGCATGTTGGTGA 414
DB 242 CAGAAACCATTTGAGTGAGGAGAAACCAATGCTTAACAAAGTATGATGCTGCTGGG 301
QY 415 ACAGAGAGAAATGTTTGGCTGCAGAAACCTGTCTACCAAGAAAGTATCAAGC 474
DB 302 ACCAGAGATTAATGTTTGGCTGCAGAAACCTGTCTACCAAGAAAGTATCAAGC 361
QY 475 AATGCAAGCCATACCATTAAGAGCTGCTTCCATGACAGCCAGAGGCTGTATTAATGA 534
DB 362 AATGCAAGCTTATACCAAAAGCTGCTTCAATGATGATGAGAGTGTATGATCAGC 421
QY 535 CCTTCCAACTATACCGCATGAGGCGCTTATATTTGTAACATCAACCATATTTCACTT 594
DB 422 CCATCAAACTATATTTGCGATGAAGGCTGCTTACAGACAGACACCAACCAACTC 481
QY 595 ATCAAGGAGAAAGGCAACTTAAGCAAGCTTGAAGGCTGAC 634
DB 482 ATCAAGGAGAAAGGCTTAACCTGAGCCAGCTGAGGCTGAC 521
RESULT 5
LOCUS BQ148732 645 bp mRNA linear EST 24-Apr-2002
DEFINITION NF080H09FL11080 Developing flower Medicago truncatula cDNA clone
ACCESSION BQ148732
VERSION BQ148732.1 GI:20285791
KEYWORDS EST.
SOURCE Medicago truncatula
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 645)
AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL Medicago truncatula flower library
COMMENT Unpublished (2001)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 645 Std Error: 0.00

Plate: 080 row: H column: 09
Seq primer: TCACACGAGAAACAGCTATGAC.
FEATURES
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1..645
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/db_xref="taxon:3880"
/clone="NF080H09FL"
/clone_1id="Developing flower"
/tissue_type="Developing flowers"
/dev_stage="Developmentally pooled. Contains a mixture of
very young, developing, fully-opened flowers and flowers
in early transition into pods."
/note="Vector: Lambda Zap; cDNA was prepared from polyA+
enriched, pooled samples of equivalent amounts of total
RNA from very young, developing, fully-opened flowers and
flowers transitioning into pods. The cDNA was
directionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the Gigapack III Gold
packaging extracts. Phagemids containing cDNA inserts were
in vivo excised from the recombinant Uni-Zap XR vector
using EXAssist helper phage and the E. coli strain
XL1-Blue MRF' (Stratagene). Excised plasmids were plated
using SOLR cells."

BASE COUNT 230 a 114 c 143 g 158 t
ORIGIN
Query Match 36.5%; Score 360.2; DB 14; Length 645;
Best Local Similarity 77.3%; Pred. No. 2e-78;
Matches 437; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
QY 100 ATGCGTTTGCAGAGAACCAACAGAAATGATGGCATGTGACAGACTGTCTATCTGCTT 159
DB 34 ATGCGATTTGCAGAGAACCAACAGAAATGATGGCATGTGACAGAAACAGTTATCTTGT 93
QY 160 GACAAATTAATGCAAGTAAGAAAGATCTATACCAAAAGCTTTTCAATGCTGATCAGT 219
DB 94 GATAGATTAATGCTGTAATTAATTAATTTTCCAAAGCTTTTTCAGATTTGACACAGTGC 153
QY 220 AAGGCACTGTCAAGCTTGCAGACTACAAATCTTTGAGGAGTTCATCTATCTGATAGACA 279
DB 154 AAAGAAACCTCAAGCTTGAAGCACTACAAATCTTTTGAAGGAGTCTTTACTGACAGACA 213
QY 280 CACTTTGATCAGCTCTTCAAAACAAAGCTGAGTTGATTAAGCTTTGAAGGTACACCA 339
DB 214 CACTTGCACCAAGCTTTCAAAAGAAAGTGTAGCTTGAAGAAAGCTTTGAAGGACACCG 273
QY 340 AAAATGTGAAGCCACAGAAACCAATGACAGTGAAGAAACCAAGTACCAAGTACCA 399
DB 274 AAAATGTGAAGCCACAGAAAGTATGATATGAGAAACCTGTGACGCTAAGAGCTCA 333
QY 400 AGCATGTTTGGTGAACAGAGAGAAATGTTTGGCTGACAGAAACCTGTCTACCAACA 459
DB 334 AGTATGTTTGGTGAACAGAGGACAAATGTTTGGTGTGCAAAACAGTATACCAACT 393
QY 460 GAAAGATATCAGCAATGCGACCCATACCATTAAGAGCTGCTTCAATGACAGCCACGGA 519
DB 394 GAGAAAGTTTACAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 453
QY 520 GGCTGTGAATTAAGCCCTTCCAACTTAACCGCAATAGAGGGGCGCTTAATTTGAACAT 579
DB 454 GGGTGTACTATCAAGTCTCTTCCAAATTAATGACATAGAGGAAACCTGCTACTGCAACAC 513
QY 580 CACCATTTCAACTATTAAGAGAGAGAGGCAACTTAAGCAAGCTTGAAGGAGTACCATGAA 639
DB 514 CACCATTTCAACTATTAAGAGAGAGAGGCAAAATTAAGCCAGCTAAGAGGTGACCATGAG 573
QY 640 ATGAATTCACAGACACACAGAG 664
DB 574 AAAATGCTGGAATAATCAATGTG 598
RESULT 6
BQ857598

FEATURES	Location/Qualifiers
source	1. .690

Query Match	36.48;	Score 360;	DB 14;	Length 690;
Best Local Similarity	80.88;	Pred. No. 2.3e-78;		

QY	175	GATAACAGATCTATCACAAGCTTTGTTTCAGANTGCCATCCTGCAAGGCACTGTCAAG	234
Db	61	GATAATCCGATCTTCCACAAGCTTGCTTCAGATGCCACCATTCGAATGCAACCTCCAAAG	120
QY	235	CTTGGCACTACAAATTTCTTTGAGGGAATTCTATACTGTAGACCACTTTTATAGCTC	294
Db	121	CTTAGCAACTACAACTCCCTTTGAGGGAGATTCTGTATTTCCAGGCCACACTTTGATCAACTC	180
QY	295	TTTCAACCAAACTGGCAGTTTGGATTAAAGCTTTGAAGGATCACCAAAAAATGTGAAGCA	354
Db	181	TTTCGGAAGACTGGTAGCTTAGACAAAGACCTTTGAAGGCACCCCAAGAATTTTGAAGCCA	240

RESULT 7	AM559538	782 bp	mRNA	linear	EST 07-SEP-2000
LOCUS	AM559538				
DEFINITION	AM559538	DSIR	Medicago truncatula	CDNA clone	PDSIR-19N4, mRNA
ACCESSION	AM559538				
VERSION	AM559538.1	GI:7204964			
KEYWORDS	EST.				
SOURCE	barrel medic.				
ORGANISM	Medicago truncatula				

REFERENCE	AUTHORS	TITLE	JOURNAL COMMENT
I (bases 1 to 782)	Pedotoro,M., Pierston,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.	ESTs from roots of Medicago truncatula after inoculation with Phytophthora medicaginis	Published (1999) Contact: Carroll P. Vance
		Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.	

Department of Agronomy and Plant Genetics
University of Minnesota
411 Borling Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
Email: vancec004@maroon.tc.umn.edu
Minnesota EST name: M250824e; TIGR sequence name: MTBAL74TK. More
information, including clone ordering, is available at: .
'http://chrvisc.tamu.edu/medicago/
Seq primer: SKmod (CTA gAA CTA gTg GAT CC).
Location/Qualifiers
I. .782

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/organism="Medicago truncatula"
/cultivar="genotype A17"
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medicaginis"
/dev_stage="roots harvested at 10 days post inoculation
with Phytophthora medicaginis"
/lab_host="E. coli strain XL0LR"
/notice="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10 days post inoculation with
Phytophthora medicaginis. The cDNA was directionally
ligated into the uni-zap XR vector from Stratagene and
packaged using Gigapack III Gold packaging extracts.
Plasmids containing cDNA inserts were excised from the
recombinant Lambda-zap phage using Ex-Assist helper phage

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RESULT 9
LOCUS      B1129342
DEFINITION G089P41Y Populus cambium cDNA library Populus tremula x Populus
            tremuloides cDNA, mRNA sequence.
ACCESSION  B1129342
VERSION    B1129342.1
KEYWORDS   GI:18013313
SOURCE     Populus tremula x Populus tremuloides.
            Populus tremula x Populus tremuloides.
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE  1 (bases 1 to 538)
AUTHORS   Herzig, M., Aspberg, H., Erlandsson, R., Bjorkbacka, H., Hiltunen,
            T., Kallsson, J., Teeri, T., Gustafsson, P., Bahlario, R., Jansson, S.,
            Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M., Sandberg, G. and
            Lundberg, U.
TITLE      Gene expression in Populus
JOURNAL    Unpublished (2001)
COMMENT    Contact: Erlandsson R
            Department of Biotechnology
            Royal Institute of Technology
            Teknikringen 30, Stockholm S-10044, Sweden
            Tel: 46 8 790 8287
            Fax: 46 8 245452
            Email: rikert@biochem.kth.se.
FEATURES   Location/Qualifiers
            source             1..538
                                /organism="Populus tremula x Populus tremuloides"
                                /db_xref="taxon:47664"
                                /clone_lib="Populus cambium cDNA library"
                                /note="Organ: cambium"
BASE COUNT 170 a 123 c 114 g 131 t
ORIGIN
Query Match 33.7%; Score 333.2; DB 13; Length 538;
Best Local Similarity 79.3%; Pred. No. 9.3e-72;
Matches 395; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 99 CATTGGCTTTGCGAGAACCCACACAGAAATGATGGATGGACAGACTGTCTATCTGCT 158
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DB 41 CATTGGCTTTGCGAGAACCCACACAGAAATGATGGATGGACAGACTGTCTATCTGCT 100
QY 159 TGAACAATTACGACAGATATCTATCAAAAGCTGTTTCAGATGCCATCTG 218
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DB 101 GACACAGTTTACGACGCTGATATACCGTGTGTACACAGAGCTTGCTCGATGCCATCTAT 160
QY 219 CAAGGACACTGTCAAGCTTGGCACTACATTCCTTTGAGGAGTTCTATCTATCTAGACC 278
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DB 161 CAGAGAACCTTCAAGCTTGGCACTACATTCCTTTGAGGAGTTCTATCTATCTAGACC 220
QY 279 ACATTTGATGACCTCTTCAACAACACTGGCAGTTTGGATTAAGCTTTGAAGTACACC 338
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 221 ACATTTGATGACCTCTTCAACAACACTGGCAGTTTGGATTAAGCTTTGAAGTACACC 280
QY 339 AAAAATTTGAACACACAGAAACCATTTGACAGTGAAGAACCAAGTACCAAGTAC 398
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DB 281 AAAAATTTGAACACACAGAAACCATTTGACAGTGAAGAACCAAGTACCAAGTAC 340
QY 399 AACGATGTTTGTGGAACAGAGAAATGTTTGGCTGCAAGAAATGCTTACCCAC 458
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DB 341 GACGATGTTTGTGGAACAGAGAAATGTTTGGCTGCAAGAAATGCTTACCCAC 400
QY 459 AGAAAGGCTATCGACCAATGGCAGCCATACCTAAGAGCTGCTTCCATATGCAAGCCAG 518
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 401 TGGAGAGGTTTGGCTGATGGAACCTCTTACCAAAAGCTGCTCAAAATGCAATTCATGG 460
QY 519 AGGCTGTGTAATAGCCCTTCAACTATACGACATGAGGGGCGCTATATGTAACA 578
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DB 461 AGCATGTACATTAAGCCATCACTACATTCATGCAATGAAGGTGCGCTTACTGCAACA 520

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QY 579 TCACCATATTCACACTAT 596
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DB 521 CCACACACACCACTAT 538
RESULT 10
LOCUS      BG043927
DEFINITION BG043927
            sa34h07.y1 Gm-cl059 Glycine max cDNA clone GENOME SYSTEMS CLONE
            ID: Gm-cl059-1118 5', similar to TR:Q9SP54 Q9SP54 LIM DOMAIN PROTEIN
            LIM1.1, mRNA sequence.
ACCESSION  BG043927
VERSION    BG043927.1
KEYWORDS   GI:12490407
SOURCE     soybean.
            Glycine max
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE  1 (bases 1 to 593)
AUTHORS   Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Coryell, V., Khana,
            A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
            Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers,
            Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk,
            R., Ritzer, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann,
            R., Waterston, R. and Wilson, R.
TITLE      Public Soybean EST Project
JOURNAL    Unpublished (1999)
COMMENT    Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@wustl.edu
            This clone is available through: Resgen, Invitrogen Corp. 2130
            South Memorial Parkway Huntville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: cun@resgen.com
            High quality sequence stop: 418.
FEATURES   Location/Qualifiers
            source             1..593
                                /organism="Glycine max"
                                /db_xref="taxon:3847"
                                /clone="GENOME SYSTEMS CLONE ID: Gm-cl059-1118"
                                /clone_lib="Gm-cl059"
                                /issue_type="Whole seedling, 2 week old, etiolated"
                                /lab_host="DH10B"
                                /note="Vector: Bluescript II SK+; Site_1: EcoRI; Site_2:
                                XhoI; The cDNA library was constructed from mRNA isolated
                                from 2 week old etiolated whole seedlings of P1468916.
                                Complementary DNA was synthesized from mRNA using a primer
                                consisting of a poly(dt) sequence with a XhoI restriction
                                site. EcoRI adapters were ligated to the blunt-ended cDNA
                                fragments followed by XhoI digestion. The cDNA fragments
                                were directionally cloned into the EcoRI- XhoI restriction
                                site of the pBluescript vector. The ligated cDNA fragments
                                were transformed into DH10B host cells (Gibco BRL). This
                                library was constructed in the laboratory of Dr. Randy
                                Shoemaker at Iowa state university."
BASE COUNT 205 a 122 c 136 g 130 t
ORIGIN
Query Match 33.4%; Score 330.4; DB 12; Length 593;
Best Local Similarity 76.5%; Pred. No. 4.7e-71;
Matches 419; Conservative 0; Mismatches 126; Indels 3; Gaps 1;
QY 100 ATGCGCTTTTCAGAGAACACAGAAATGATGGATGGACAGACTGTCTATCTGCT 159
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DB 21 ATGCGATTTTCAGAGAACACAGAAATGATGGATGGACAGACTGTCTATCTGCT 80
QY 160 GACAAATTAACCTGCAGATTAACAGAAATCTATTCACAAAGCTTGTTCAGATGCCATCTGC 219

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Db      81 GATAGCTTGACCCGAGATAACCGAGTACCATTAAGCGCTTGCAGATGCACCACTGC 140
QY      220 AAGGCACTGTCAGCTGGCACTACATTCCTTTAGGAGGATCTTACTGTAGACCA 279
Db      141 AAGGAACACTCAAGCTCAGCACTATTAATCTTTGAGGAGTCTTACTGACAGCCA 200
QY      280 CACTTTGATCAGCTCTTCAAAACAACCTGGCAGTTTGGTAAAGCTTTGAAGTACACA 339
Db      201 CACTTTGACCACTGTTCAAAAGAAGTGTGTCTTGAACAAAGCTTGAAGGACACCA 260
QY      340 AAAATGTGAAGCCACAGAAACCATTTGACAGTACAGAACCCAGCTAACCAAGTACA 399
Db      261 AAAATCTCTAAACCGAAGAAAACCGGGA---AGAGAAACCTGCAGCAACCAAGTCTCA 317
QY      400 AGCATGTTGGTGGACAGAGAGAAGATGTTTGGCTGCAGAAAGCTGTACCAACA 459
Db      318 AGTATGTTGGTGGTGAAGTACAGATTAATGTGGGGTGTGCAAGAAAGTGTATCCACT 377
QY      460 GAAAGGTATCAGCAATGGCAGCCATACCATTAAGAGCTGCTTCAATGCAGCCACGCA 519
Db      378 GAAAGGTATCAGCTGATGGAAGTACCTTTATCAGAAAGTGTCTTCAATGCACATGCA 437
QY      520 GCGTGTATTAAGCCCTTCCACTATACCGACATAGAGGGCGCTTATATTTAAACAT 579
Db      438 GGGTGTATTAATGCTCCCTCCACTACATGACACAGCAAGCAACCTACTGCAGACAC 497
QY      580 CACCATTTCACTTATCAAGGAGAGAGGCACTTAAGCAAGCTTGAGGGTGACCAATGAA 639
Db      498 CACCATTTCACTGATCAAGAGAGAGGCAATTAAGCAAGCTTGAGGATGACATGAG 557
QY      640 ATGAAATTC 647
Db      558 AAGAGTAC 565

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RESULT 11      548 bp mRNA linear EST 04-DEC-2001
BE440655      sr50603.y1 Gm-cl043 glycine max cDNA clone GENOME SYSTEMS CLONE ID:
LOCUS          Gm-cl043-1662 5' similar to TR:092TN6 Q92TN6 PG9PB. ;, mRNA
DEFINITION    sequence.
ACCESSION     BE440655.1 GI:9440145
VERSION       BE440655
KEYWORDS      soybean.
SOURCE        Glycine max
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
               Glycine.

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REFERENCE      1 (bases 1 to 548)
AUTHORS        Shoemaker,R., Kelm,P., Vodkin,L., Erpellding,J., Coryell,V., Khanna
               A., Bolla,B., Matra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
               Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
               Y.L., Person,B., Swaller,T., Gibbons,M., Pape,D., Halvey,N., Schurk
               R., Rifter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
               R., Waterston,R. and Wilson,R.
TITLE          Public Soybean EST Project
JOURNAL        Unpublished (1999)
COMMENT        Contact: Shoemaker R/public Soybean EST Project
               Public Soybean EST Project
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
               Tel: 314 286 1800
               Fax: 314 286 1810

```

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FEATURES
Email: estewatson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact via email: couetresgen.com
Insert Length: 703 Std Error: 0.00
High quality sequence stop: 478.
Location/Qualifiers

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source
1. 548
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl043-1662"
/lssue_type="Hypocotyl and Plumule, germinating seeds"
/lab_host="Dh10B"
/notes="Vector: pT73Pac (Pharmacia); Site 1: EcoRI;
Site 2: NotI. This cDNA library was constructed from mRNA
isolated from hypocotyl and plumule tissues of seeds
germinated for three days of the cultivar Williams.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a NotI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by digestion with EcoRI and NotI. The
cDNA fragments were directionally cloned into the
EcoRI-NotI restriction site of the pT73-Pac vector. The
ligated cDNA fragments were transformed into DH10B host
cells (Gibco BRL). This library was constructed by Dr.
Randy Shoemaker."
BASE COUNT 186 a 114 c 123 g 124 t 1 others
ORIGIN
Query Match 33.1%; Score 326.8; DB 10; Length 548;
Best Local Similarity 76.6%; Pred. No. 3.6e-70;
Matches 413; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

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QY      100 ATGCGCTTTGCGAGAACCAACAGAAATGCATGTGACAAAGACTGTCTATCTGTT 159
Db      12 ATGCGCATTTGCGAGAACCAACAGAAATGCATGTGACAAAGACTGTCTATCTGTT 71
QY      160 GACAAATTAAGTGCAGATTAACAGAAATCTATCACAAAGCTGTTTGCATGCCATCACTGC 219
Db      72 GATAGCTTGACAGAGATTAACCGAGTGTACCATTAAGCTTGTCTGATGTCCACCACTGC 131
QY      220 AAGGCACTGTCAAGCTTGGCACTACATTCCTTTGAGGAGTCTTACTGTAGACCA 279
Db      132 AAGGAACACTCAAGCTTACCACTATTAATCTTTGAGGGGCTTCTTACTGCAGACCA 191
QY      280 CACTTTGATCAGCTCTTCAAAACAACCTGGCAGTGTGATTAAGCTTGAAGGTACACCA 339
Db      192 CACTTTGACCAACTGTTCAAAAGAAGTGTGTGACAAAGCTTGAAGGTACACCA 251
QY      340 AAAAATGTGAAGCCACAGAAACCCATTGACAGTGAAGAACCCAGTACGCAAAAGTGACA 399
Db      252 AAAATTTCTAAACCGAAGAAAACCGGGA---AGAGAAACCTGCAGCAACCAAGTCTCA 308
QY      400 AGCATGTTGGTGGACAGAGAGAAATGTTTGGCTGCAAGAAACCTGTACTCCACACA 459
Db      309 AGTATGTTGGTGGACAGATTAATGTGCCGCTGTCAAAAACAGGTATCCCACT 368
QY      460 GAAAGGTATCAGCAATGGCAGCCATACCATTAAGAGTGTCTTCAATGCAGCCACGCA 519
Db      369 GAAAGGTATCAGTGAAGTGAACCTCTTATCAGAAAGTGTCTTCAATGCACCTACCTGCA 428
QY      520 GCGTGTATTAAGCCCTTCCACTATACCGACATAGAGGGCGCTTATTTGAACAT 579
Db      429 GGGTGTATTAAGTGTCTTCCACTACATTTGACAGAGCAACCAACTTACTGCAAGCAC 488
QY      580 CACCATTTCACTTATCAAGAGAGAGGCACTTAAGCAAGCTTGAGGGTGAACATGA 638
Db      489 CACCATTTCACTGATCAAGAGAGAGGCAATTAAGTGAAGCAACTTGAAGCTGACATGA 547

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RESULT 12      589 bp mRNA linear EST 17-JUL-2002
LOCUS          B0741219
DEFINITION    sag15g09.y1 Gm-cl045 glycine max cDNA clone SOYBEAN CLONE ID: 5'
               similar to TR:Q9SP54 Q9SP54 LIM DOMAIN PROTEIN WLIM1. ;, mRNA
               sequence.
ACCESSION     B0741219
VERSION       B0741219.1 GI:21888006
KEYWORDS      EST.

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Source	Organism
soybean	Glycine max
Euariotata	Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine
REFERENCE	1 (bases 1 to 589)
AUTHORS	Shoemaker, R., Kaim, P., Vodkin, L., Erpelidg, J., Corryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Peterson, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritten, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
TITLE	Public Soybean EST Project
JOURNAL	Unpublished (1999)
COMMENT	Contact: Shoemaker R./Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com Seq primer: -40RP from Glibco High quality sequence stop: 431. Location/Qualifiers 1. 589 /organism="Glycine max" /db_xref="taxon:3847" /clone="SOYBEAN CLONE ID:" /clone_1id="Gm-cl045" /tissue.type="Hypocotyl, 9-10 day old etiolated seedlings" /lab_host="DH10B" /note="Vector: pluescriptII SK+, Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from etiolated hypocotyl tissue of 9-10 day old seedlings of the cultivar Williams 82. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) primer with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and XhoI. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."
BASE COUNT	199 a 127 c 127 g 136 t
ORIGIN	
Query Match	31.7%; Score 313.2; DB 14; Length 589;
Best Local Similarity	73.3%; Pred. No. 8.3e-67;
Matches	415; Conservative 0; Mismatches 148; Indels 3; Gaps 1;
49	AGAGCACAAGACCATTTTGTTCCTGTAACCTCTGTATATAGCCATGGCTTT 108
27	ACACACAAAGGATCATATATCTTGTTGCACCTGTGAAGGTGAGAAATATGCAATTT 86
109	GCAGAACACACACAGAAATGCATGGCAGTGTGACAGACTGCTATCTGTTGACAATTA 168
87	GCAGGAAACACACAGAAATGCATGGCTGTGACAAACAGTTATCTGTTGATTAAGTTG 146
169	ACTGAGATTAACAGAAATGATATACCAAACTGTTTCACATGGCATTCGCAAGGCACT 228
147	ACCGCAGATTAACCGAGTGTACCATTAAGCTTGCTTCAATGACACATGCAAGGAACA 206
229	GTCACGCTTGACATACAAATTCCTTTTGAAGGAGTTCTATACCTGTAGACACACTTTGAT 288
207	CTCAAGCTCAGACAACTATTAACCTTTTGAAGAGTCTTTACTGCAAGGCACACTTTGAC 266
289	CAGCTCTTCAACAACTGCGCAGTTTGGATTAAGCTTTGAAGTACCAACCAAAAATGTG 348

Db	Accession	Version	Keywords	Organism	Title	Reference	Authors	Journal	Comment	Features	Source
Db	267	CAACTGTTCAAAAGACACTGTA	656 bp	Citrus sinensis	Expressed sequence tags isolated from entire sweet orange (C. sinensis L. Osbeck) seedling	Bausher, M., McKendree, W., Dang, P., Chaparro, J., Shatters, R., Hunter, W. and Nied, R.	USDA - ARS	2001 South Rock Rd., Fort Pierce, FL 34945, USA	Tel: (772) 462-5918 Fax: (772) 462-5961 Email: mbausher@usshr.ars.usda.gov	Seq primer: T3 primer. Location/Qualifiers 1..656 /organism="Citrus sinensis" /cultivar="Ridge Pineapple" /db_xref="taxon:2711 /clone_1lb="USDA-FP_00542" /clone_1lb="Ridge pineapple sweet orange entire seedling" /tissue_type="entire seedling" /dev_stages="50 days after germination" /lab_host="XLI-Blue"	ORIGIN
Db	349	AAGCCACAGAAACCCATTGACAGT	656 bp	Citrus sinensis	Expressed sequence tags isolated from entire sweet orange (C. sinensis L. Osbeck) seedling	Bausher, M., McKendree, W., Dang, P., Chaparro, J., Shatters, R., Hunter, W. and Nied, R.	USDA - ARS	2001 South Rock Rd., Fort Pierce, FL 34945, USA	Tel: (772) 462-5918 Fax: (772) 462-5961 Email: mbausher@usshr.ars.usda.gov	Seq primer: T3 primer. Location/Qualifiers 1..656 /organism="Citrus sinensis" /cultivar="Ridge Pineapple" /db_xref="taxon:2711 /clone_1lb="USDA-FP_00542" /clone_1lb="Ridge pineapple sweet orange entire seedling" /tissue_type="entire seedling" /dev_stages="50 days after germination" /lab_host="XLI-Blue"	ORIGIN
Db	327	AAACCCAGAAAAACCGGGGA---	656 bp	Citrus sinensis	Expressed sequence tags isolated from entire sweet orange (C. sinensis L. Osbeck) seedling	Bausher, M., McKendree, W., Dang, P., Chaparro, J., Shatters, R., Hunter, W. and Nied, R.	USDA - ARS	2001 South Rock Rd., Fort Pierce, FL 34945, USA	Tel: (772) 462-5918 Fax: (772) 462-5961 Email: mbausher@usshr.ars.usda.gov	Seq primer: T3 primer. Location/Qualifiers 1..656 /organism="Citrus sinensis" /cultivar="Ridge Pineapple" /db_xref="taxon:2711 /clone_1lb="USDA-FP_00542" /clone_1lb="Ridge pineapple sweet orange entire seedling" /tissue_type="entire seedling" /dev_stages="50 days after germination" /lab_host="XLI-Blue"	ORIGIN
Db	409	GGTGGACACAGAGAAATGTTTGG	656 bp	Citrus sinensis	Expressed sequence tags isolated from entire sweet orange (C. sinensis L. Osbeck) seedling	Bausher, M., McKendree, W., Dang, P., Chaparro, J., Shatters, R., Hunter, W. and Nied, R.	USDA - ARS	2001 South Rock Rd., Fort Pierce, FL 34945, USA	Tel: (772) 462-5918 Fax: (772) 462-5961 Email: mbausher@usshr.ars.usda.gov	Seq primer: T3 primer. Location/Qualifiers 1..656 /organism="Citrus sinensis" /cultivar="Ridge Pineapple" /db_xref="taxon:2711 /clone_1lb="USDA-FP_00542" /clone_1lb="Ridge pineapple sweet orange entire seedling" /tissue_type="entire seedling" /dev_stages="50 days after germination" /lab_host="XLI-Blue"	ORIGIN
Db	384	GGTGGAACTAGAGATTAATGTCG	656 bp	Citrus sinensis	Expressed sequence tags isolated from entire sweet orange (C. sinensis L. Osbeck) seedling	Bausher, M., McKendree, W., Dang, P., Chaparro, J., Shatters, R., Hunter, W. and Nied, R.	USDA - ARS	2001 South Rock Rd., Fort Pierce, FL 34945, USA	Tel: (772) 462-5918 Fax: (772) 462-5961 Email: mbausher@usshr.ars.usda.gov	Seq primer: T3 primer. Location/Qualifiers 1..656 /organism="Citrus sinensis" /cultivar="Ridge Pineapple" /db_xref="taxon:2711 /clone_1lb="USDA-FP_00542" /clone_1lb="Ridge pineapple sweet orange entire seedling" /tissue_type="entire seedling" /dev_stages="50 days after germination" /lab_host="XLI-Blue"	ORIGIN
Db	469	TCAGCCATGAGAGCCCATACCAT	656 bp	Citrus sinensis	Expressed sequence tags isolated from entire sweet orange (C. sinensis L. Osbeck) seedling	Bausher, M., McKendree, W., Dang, P., Chaparro, J., Shatters, R., Hunter, W. and Nied, R.	USDA - ARS	2001 South Rock Rd., Fort Pierce, FL 34945, USA	Tel: (772) 462-5918 Fax: (772) 462-5961 Email: mbausher@usshr.ars.usda.gov	Seq primer: T3 primer. Location/Qualifiers 1..656 /organism="Citrus sinensis" /cultivar="Ridge Pineapple" /db_xref="taxon:2711 /clone_1lb="USDA-FP_00542" /clone_1lb="Ridge pineapple sweet orange entire seedling" /tissue_type="entire seedling" /dev_stages="50 days after germination" /lab_host="XLI-Blue"	ORIGIN
Db	444	ACCGGAATGAGACCTCTTATCAG	656 bp	Citrus sinensis	Expressed sequence tags isolated from entire sweet orange (C. sinensis L. Osbeck) seedling	Bausher, M., McKendree, W., Dang, P., Chaparro, J., Shatters, R., Hunter, W. and Nied, R.	USDA - ARS	2001 South Rock Rd., Fort Pierce, FL 34945, USA	Tel: (772) 462-5918 Fax: (772) 462-5961 Email: mbausher@usshr.ars.usda.gov	Seq primer: T3 primer. Location/Qualifiers 1..656 /organism="Citrus sinensis" /cultivar="Ridge Pineapple" /db_xref="taxon:2711 /clone_1lb="USDA-FP_00542" /clone_1lb="Ridge pineapple sweet orange entire seedling" /tissue_type="entire seedling" /dev_stages="50 days after germination" /lab_host="XLI-Blue"	ORIGIN
Db	529	ATAAGCCCTTCCCACTATACGCA	656 bp	Citrus sinensis	Expressed sequence tags isolated from entire sweet orange (C. sinensis L. Osbeck) seedling	Bausher, M., McKendree, W., Dang, P., Chaparro, J., Shatters, R., Hunter, W. and Nied, R.	USDA - ARS	2001 South Rock Rd., Fort Pierce, FL 34945, USA	Tel: (772) 462-5918 Fax: (772) 462-5961 Email: mbausher@usshr.ars.usda.gov	Seq primer: T3 primer. Location/Qualifiers 1..656 /organism="Citrus sinensis" /cultivar="Ridge Pineapple" /db_xref="taxon:2711 /clone_1lb="USDA-FP_00542" /clone_1lb="Ridge pineapple sweet orange entire seedling" /tissue_type="entire seedling" /dev_stages="50 days after germination" /lab_host="XLI-Blue"	ORIGIN
Db	504	ATTAGTCCCTCCCACTATACGCA	656 bp	Citrus sinensis	Expressed sequence tags isolated from entire sweet orange (C. sinensis L. Osbeck) seedling	Bausher, M., McKendree, W., Dang, P., Chaparro, J., Shatters, R., Hunter, W. and Nied, R.	USDA - ARS	2001 South Rock Rd., Fort Pierce, FL 34945, USA	Tel: (772) 462-5918 Fax: (772) 462-5961 Email: mbausher@usshr.ars.usda.gov	Seq primer: T3 primer. Location/Qualifiers 1..656 /organism="Citrus sinensis" /cultivar="Ridge Pineapple" /db_xref="taxon:2711 /clone_1lb="USDA-FP_00542" /clone_1lb="Ridge pineapple sweet orange entire seedling" /tissue_type="entire seedling" /dev_stages="50 days after germination" /lab_host="XLI-Blue"	ORIGIN
Db	589	CAACTTATCAAGAGAGAGGCACT	614	Citrus sinensis	Expressed sequence tags isolated from entire sweet orange (C. sinensis L. Osbeck) seedling	Bausher, M., McKendree, W., Dang, P., Chaparro, J., Shatters, R., Hunter, W. and Nied, R.	USDA - ARS	2001 South Rock Rd., Fort Pierce, FL 34945, USA	Tel: (772) 462-5918 Fax: (772) 462-5961 Email: mbausher@usshr.ars.usda.gov	Seq primer: T3 primer. Location/Qualifiers 1..614 /organism="Citrus sinensis" /cultivar="Ridge Pineapple" /db_xref="taxon:2711 /clone_1lb="USDA-FP_00542" /clone_1lb="Ridge pineapple sweet orange entire seedling" /tissue_type="entire seedling" /dev_stages="50 days after germination" /lab_host="XLI-Blue"	ORIGIN
Db	564	CAACTGATCAAGAGAGAGGCACT	589	Citrus sinensis	Expressed sequence tags isolated from entire sweet orange (C. sinensis L. Osbeck) seedling	Bausher, M., McKendree, W., Dang, P., Chaparro, J., Shatters, R., Hunter, W. and Nied, R.	USDA - ARS	2001 South Rock Rd., Fort Pierce, FL 34945, USA	Tel: (772) 462-5918 Fax: (772) 462-5961 Email: mbausher@usshr.ars.usda.gov	Seq primer: T3 primer. Location/Qualifiers 1..589 /organism="Citrus sinensis" /cultivar="Ridge Pineapple" /db_xref="taxon:2711 /clone_1lb="USDA-FP_00542" /clone_1lb="Ridge pineapple sweet orange entire seedling" /tissue_type="entire seedling" /dev_stages="50 days after germination" /lab_host="XLI-Blue"	ORIGIN
RESULT 13	B062345										

Db 65 ATGCATCACCCTTTGGAGGAAACCAACAAAATGATGCCCTGTGACAAACCTGTGAC 124
QY 154 CTGGTTGCAAAATTTAACTGACAGATTAACAAATCTATCAACAAAGCTTGTTCAGATGCCAT 213
Db 125 CTGTGTGTAAGTTAGGCGCGATTAATGGGCTCTATCAACAAAGCTTGTTCAGATGCCAC 184
QY 214 CACTGCAAGGCACTGTCAAGCTTGGCACTACATCAATTCCTTTGAGGAGGAGTCTATACGT 273
Db 185 CATTGCAAGGCAACCTTCACAGCTCAACCTTCATTCCTTTGAGGAGGAGTCTATACGT 244
QY 274 AGACGACCTTTGATGATCTCTTCAACAACTGGCAGTTGGATTAACAAAGCTTGAAGCT 333
Db 245 AGGCTCTACTTTGATGATCTCTTCAAGAGAACTGGCAGCTGGAGAAAGATTTTGAAGGA 304
QY 334 ACACCAAAATTTGTAAGGCAACAGAAACCACTTGCAGTGAAGAAACAGATCAACCA 393
Db 305 ACACCAAAATTTGTAAGGCAACAGAAACCACTTGCAGTGAAGAAAGATCAACCA 358
QY 394 GTGACAGCAGTGTGTGTGGAACAAGAAATGTTTGGCTGCAGAAACCTGTCTAC 453
Db 359 GTCTCCAAAGTTGTGTGGCAGCAGAGATTAATGTGTGGATGGATAGGACTGTAT 418
QY 454 CCACAGAAAGGATATCGCAATGGCAGCAGATTCATTAAGATGCTGTCCATGACAGC 513
Db 419 CCAACTGAAAGGTTCTGTAAATGGCGCCGATATATAGGAGCTGTCAAGTGCAGC 478
QY 514 CACGAGGCTGTGTAATAGCCCTTCCAACTATACCCGACATGAGGAGGCTTATATGT 573
Db 479 CATGAGGCTGTGTAATAGCCCTTCCAACTATATATGTCGCAAGGAGAACTGTACG 538
QY 574 AAACATGACCAATTTCACTTATCAAGAGAAAGGCACTTAAGCAAGCTTGAAGGTGAC 633
Db 539 AAGCATCATCAATACACTCTTCAGAGAGAAAGAACTACAGCCAGCTGAGAGTGAT 598
QY 634 CATGAATGAAT 645
Db 599 CTGAGAGAGT 610

RESULT 14
BF638624
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF638624 657 bp mRNA linear EST 19-DEC-2000
NM062F05PL1F1045 Phosphate starved leaf Medicago truncatula cDNA
BF638624
BF638624.1 GI:11902782
EST.
barrel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 657)
AUTHORS
TITLE
JOURNAL
COMMENT

Liu,D., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
Unpublished (2000)
Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 657 Std Error: 0.00
Plate: 062 row: F column: 05
Seq primer: TCACACGAAACAGCATATC.
location/Qualifiers
1..657
/organism="Medicago truncatula"
/db_xref="taxon:3880"

/clone="NF062F05PL"
/clone_id="phosphate starved leaf"
/tissue_type="leaf"
/day_stage="trifoliolate"
/note="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoagland solution containing only 20um potassium
phosphate. RNA was prepared from above ground tissues."

BASE COUNT 211 a 122 c 125 g 192 t 7 others
ORIGIN

Query Match 31.4%; Score 310.2; DB 12; Length 657;
Best Local Similarity 77.7%; Pred. No. 4.7e-66;
Matches 383; Conservative 0; Mismatches 109; Indels 1; Gaps 1;

QY 100 ATGCTTTGAGAGAACCCACAGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 159
Db 166 ATGCAATTTGAGAGAACCCACAGAAATGCAATGCAATGCAATGCAATGCAATGCAAT 225
QY 160 GACAAATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 219
Db 226 GATAGTTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 285
QY 220 AAGGCACTCTCAAGCTTGCAGCAATTCCTTTGAGGAGGAGTCTATACCTGACCA 279
Db 286 AAGGCACTCTCAAGCTTGCAGCAATTCCTTTGAGGAGGAGTCTATACCTGACCA 345
QY 280 CACTTTGATCAGCTCTTCAACAACTGCGAGCTTGTGTAATTAAGCTTGAAGTACCA 339
Db 346 CACTTCGACCACTGTTCAAAAGAACTGTGAGCTTGAAGAACTTGAAGGAGCAACCG 405
QY 340 AAAATGGAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 399
Db 406 AAAATGGAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 465
QY 400 AGCATGTTTGTGAG 459
Db 466 AGTATGTTTGTGAG 525
QY 460 GAAAGGATATCAGCAATGCGAGCCATACCATTAAGAGCTGTCCAAATGACGACGCA 519
Db 526 GAGAGGATATCAGCAATGCGAGCCATACCATTAAGAGCTGTCCAAATGACGACGCA 585
QY 520 GCGTGTGAATTAAGCCCTTCCAACTATACCGCAATGAGGAGGCGCTTAATTAAGCA 579
Db 586 NGTGTACTATCACTCTTCC-ATTACATGACACATGAGGAGGAGGAGGAGGAGGAG 644
QY 580 CACCATATTCAC 592
Db 645 CACCATATTCAC 657

RESULT 15
BM178858
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM178858 535 bp mRNA linear EST 06-DEC-2001
Saj60d07.y1 Gm-c1072 Glycine max cDNA clone SOYEAN CLONE ID:
Gm-c1072-4021 5' similar to TR:Q9SP54 Q9SP54 LIM DOMAIN PROTEIN
WLM1.; mRNA sequence.
BM178858
BM178858.1 GI:17402076
EST.
soybean.
glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 535)
REFERENCE
AUTHORS

Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corryell,V., Khanna
A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers

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